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[US/US]: 440 NE 73rd Street, # 201, Seattle, WA 98103 (US).

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(74) Agents: MAKI, David, J. et al.; Seed And Berry LLP, Suite 6300, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).

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(71) Applicant (*for all designated States except US*): CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).

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(72) Inventors; and

(75) Inventors/Applicants (*for US only*): PROBST, Peter [DE/US]; 137 NW 77th Street, Seattle, WA 98117 (US). BHATIA, Ajay [IN/US]; 1805 Bellevue Ave. #204, Seattle, WA 98104 (US). SKEIKY, Yasir, A., W. [CA/US]; 15106 SE 47th Place, Bellevue, WA 98006 (US). FLING, Steven, P. [US/US]; 11414 Pinyon Avenue Northeast, Bainbridge Island, WA 98110 (US). JEN, Shyian [US/US]; 2345, 1/2 Boylston Avenue E, #201, Seattle, WA 98122 (US). STROMBERG, Erica, Jean

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WO 00/34483 A2

(54) Title: COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIALINFECTION

(57) Abstract: Compounds and methods for the diagnosis and treatment of Chlamydial infection are disclosed. The compounds provided include polypeptides that contain at least one antigenic portion of a *Chlamydia* antigen and DNA sequences encoding such polypeptides. Pharmaceutical compositions and vaccines comprising such polypeptides or DNA sequences are also provided, together with antibodies directed against such polypeptides. Diagnostic kits containing such polypeptides or DNA sequences and a suitable detection reagent may be used for the detection of Chlamydial infection in patients and in biological samples.

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## COMPOUNDS AND METHODS FOR TREATMENT AND DIAGNOSIS OF CHLAMYDIAL INFECTION

### TECHNIGAL FIELD

The present invention relates generally to the detection and treatment of Chlamydial infection. In particular, the invention is related to polypeptides comprising a *Chlamydia* antigen and the use of such polypeptides for the serodiagnosis and treatment of Chlamydial infection.

### BACKGROUND OF THE INVENTION

Chlamydiae are intracellular bacterial pathogens that are responsible for a wide variety of important human and animal infections. *Chlamydia trachomatis* is one of the most common causes of sexually transmitted diseases and can lead to pelvic inflammatory disease (PID), resulting in tubal obstruction and infertility. *Chlamydia trachomatis* may also play a role in male infertility. In 1990, the cost of treating PID in the US was estimated to be \$4 billion. Trachoma, due to ocular infection with *Chlamydia trachomatis*, is the leading cause of preventable blindness worldwide. *Chlamydia pneumonia* is a major cause of acute respiratory tract infections in humans and is also believed to play a role in the pathogenesis of atherosclerosis and, in particular, coronary heart disease. Individuals with a high titer of antibodies to *Chlamydia pneumonia* have been shown to be at least twice as likely to suffer from coronary heart disease as seronegative individuals. Chlamydial infections thus constitute a significant health problem both in the US and worldwide.

Chlamydial infection is often asymptomatic. For example, by the time a woman seeks medical attention for PID, irreversible damage may have already occurred resulting in infertility. There thus remains a need in the art for improved vaccines and pharmaceutical

compositions for the prevention and treatment of *Chlamydia* infections. The present invention fulfills this need and further provides other related advantages.

## SUMMARY OF THE INVENTION

The present invention provides compositions and methods for the diagnosis and therapy of *Chlamydia* infection. In one aspect, the present invention provides polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, or a variant of such an antigen. Certain portions and other variants are immunogenic, such that the ability of the variant to react with antigen-specific antisera is not substantially diminished. Within certain embodiments,, the polypeptide comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of (a) a sequence of SEQ ID NO: 1, 15, 21-25, 44-64, 66-76, 79-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-290; (b) the complements of said sequences; and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions. In specific embodiments, the polypeptides of the present invention comprise at least a portion of a *Chlamydial* protein that includes an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 5-14, 17-20, 26, 28, 30-32, 34, 39-43, 65, 89-109, 138-158, 167, 168, 224-262, 246, 247, 254-256, 292, and variants thereof.

The present invention further provides polynucleotides that encode a polypeptide as described above, or a portion thereof (such as a portion encoding at least 15 amino acid residues of a *Chlamydial* protein), expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

In a related aspect, polynucleotide sequences encoding the above polypeptides, recombinant expression vectors comprising one or more of these polynucleotide sequences and host cells transformed or transfected with such expression vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising an inventive polypeptide, or, alternatively, an inventive polypeptide and a known *Chlamydia* antigen, as well as polynucleotides encoding such fusion proteins, in combination with a physiologically acceptable carrier or immunostimulant for use as pharmaceutical compositions and vaccines thereof.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody, both polyclonal and monoclonal, or antigen-binding fragment thereof that specifically binds to a *Chlamydial* protein; and (b) a physiologically acceptable carrier. Within other aspects, the present invention provides pharmaceutical compositions that comprise one or more *Chlamydia* polypeptides disclosed herein, or a polynucleotide molecule encoding such a polypeptide, and a physiologically acceptable carrier. The invention also provides vaccines for prophylactic and therapeutic purposes comprising one or more of the disclosed polypeptides and an immunostimulant, as defined herein, together with vaccines comprising one or more polynucleotide sequences encoding such polypeptides and an immunostimulant.

In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above pharmaceutical compositions or vaccines.

In yet a further aspect, methods for the treatment of *Chlamydia* infection in a patient are provided, the methods comprising obtaining peripheral blood mononuclear cells (PBMC) from the patient, incubating the PBMC with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated T cells and administering the incubated T cells to the patient. The present invention additionally provides methods for the treatment of *Chlamydia* infection that comprise incubating antigen presenting cells with a polypeptide of the present invention (or a polynucleotide that encodes such a polypeptide) to provide incubated antigen presenting cells and administering the incubated antigen presenting cells to the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient. In certain embodiments, the antigen presenting cells are selected from the group consisting of dendritic cells, macrophages, monocytes, B-cells, and fibroblasts. Compositions for the treatment of *Chlamydia* infection comprising T cells or antigen presenting cells that have been incubated with a polypeptide or polynucleotide of the present invention are also provided. Within related aspects, vaccines are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, within other aspects, methods for

removing *Chlamydial*-infected cells from a biological sample, comprising contacting a biological sample with T cells that specifically react with a *Chlamydial* protein, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of *Chlamydial* infection in a patient, comprising administering to a patient a biological sample treated as described above. In further aspects of the subject invention, methods and diagnostic kits are provided for detecting *Chlamydia* infection in a patient. In one embodiment, the method comprises: (a) contacting a biological sample with at least one of the polypeptides or fusion proteins disclosed herein; and (b) detecting in the sample the presence of binding agents that bind to the polypeptide or fusion protein, thereby detecting *Chlamydia* infection in the biological sample. Suitable biological samples include whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine. In one embodiment, the diagnostic kits comprise one or more of the polypeptides or fusion proteins disclosed herein in combination with a detection reagent. In yet another embodiment, the diagnostic kits comprise either a monoclonal antibody or a polyclonal antibody that binds with a polypeptide of the present invention.

The present invention also provides methods for detecting *Chlamydia* infection comprising: (a) obtaining a biological sample from a patient; (b) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, at least one of the oligonucleotide primers being specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers. In one embodiment, the oligonucleotide primer comprises at least about 10 contiguous nucleotides of a polynucleotide sequence peptide disclosed herein, or of a sequence that hybridizes thereto.

In a further aspect, the present invention provides a method for detecting *Chlamydia* infection in a patient comprising: (a) obtaining a biological sample from the patient; (b) contacting the sample with an oligonucleotide probe specific for a polynucleotide sequence disclosed herein; and (c) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe. In one embodiment, the oligonucleotide probe

comprises at least about 15 contiguous nucleotides of a polynucleotide sequence disclosed herein, or a sequence that hybridizes thereto.

These and other aspects of the present invention will become apparent upon reference to the following detailed description. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### SEQUENCE IDENTIFIERS

SEQ ID NO: 1 is the determined DNA sequence for the *C. trachomatis* clone

1-B1-66.

SEQ ID NO: 2 is the determined DNA sequence for the *C. trachomatis* clone

4-D7-28.

SEQ ID NO: 3 is the determined DNA sequence for the *C. trachomatis* clone

3-G3-10.

SEQ ID NO: 4 is the determined DNA sequence for the *C. trachomatis* clone

10-C10-31.

SEQ ID NO: 5 is the predicted amino acid sequence for 1-B1-66.

SEQ ID NO: 6 is the predicted amino acid sequence for 4-D7-28.

SEQ ID NO: 7 is a first predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 8 is a second predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 9 is a third predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 10 is a fourth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 11 is a fifth predicted amino acid sequence for 3-G3-10.

SEQ ID NO: 12 is the predicted amino acid sequence for 10-C10-31.

SEQ ID NO: 13 is the amino acid sequence of the synthetic peptide 1-B1-

66/48-67.

SEQ ID NO: 14 is the amino acid sequence of the synthetic peptide 1-B1-

66/58-77.

SEQ ID NO: 15 is the determined DNA sequence for the *C. trachomatis* serovar LGV II clone 2C7-8

SEQ ID NO: 16 is the determined DNA sequence for a first putative open reading frame from *C. trachomatis* serovar D

SEQ ID NO: 17 is the predicted amino acid sequence encoded by the first putative open reading frame from *C. trachomatis* serovar D

SEQ ID NO: 18 is the amino acid sequence of the synthetic peptide CtC7.8-12

SEQ ID NO: 19 is the amino acid sequence of the synthetic peptide CtC7.8-13

SEQ ID NO: 20 is the predicted amino acid sequence encoded by a second putative open reading from *C. trachomatis* serovar D

SEQ ID NO: 21 is the determined DNA sequence for clone 4C9-18 from *C. trachomatis* LGV II

SEQ ID NO: 22 is the determined DNA sequence homologous to Lipoamide Dehydrogenase from *C. trachomatis* LGV II

SEQ ID NO: 23 is the determined DNA sequence homologous to Hypothetical protein from *C. trachomatis* LGV II

SEQ ID NO: 24 is the determined DNA sequence homologous to Ubiquinone Mehtyltransferase from *C. trachomatis* LGV II

SEQ ID NO: 25 is the determined DNA sequence for clone 4C9-18#2 BL21 pLysS from *C. trachomatis* LGV II

SEQ ID NO: 26 is the predicted amino acid sequence for 4C9-18#2 from *C. trachomatis* LGV II

SEQ ID NO: 27 is the determined DNA sequence for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 28 is the predicted amino acid sequence for Cp-SWIB from *C. pneumonia* strain TWAR

SEQ ID NO: 29 is the determined DNA sequence for Cp-S13 from *C. pneumonia* strain TWAR

SEQ ID NO: 30 is the predicted amino acid sequence for Cp-S13 from *C. pneumonia* strain TWAR

SEQ ID NO: 31 is the amino acid sequence for a 10mer consensus peptide from CtC7.8-12 and CtC7.8-13

SEQ ID NO: 32 is the predicted amino acid sequence for clone 2C7-8 from *C. trachomatis* LGV II

SEQ ID NO: 33 is the determined DNA sequence of a clone from *C. trachomatis* serovar D which shows homology to clone 2C7-8

SEQ ID NO: 34 is the predicted amino acid sequence encoded by the sequence of SEQ ID NO: 33

SEQ ID NO: 35 is the DNA sequence for C.p. SWIB Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 36 is the DNA sequence for C.p. SWIB EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO : 37 is the DNA sequence for C.p. S13 Nde (5' primer) from *C. pneumonia*

SEQ ID NO: 38 is the DNA sequence for C.p. S13 EcoRI (3' primer) from *C. pneumonia*

SEQ ID NO: 39 is the amino acid sequence for CtSwib 52-67 peptide from *C. trachomatis* LGV II

SEQ ID NO: 40 is the amino acid sequence for CpSwib 53-68 peptide from *C. pneumonia*

SEQ ID NO: 41 is the amino acid sequence for HuSwib 288-302 peptide from Human SWI domain

SEQ ID NO: 42 is the amino acid sequence for CtSWI-T 822-837 peptide from the topoisomerase-SWIB fusion of *C. trachomatis*

SEQ ID NO: 43 is the amino acid sequence for CpSWI-T 828-842 peptide from the topoisomerase-SWIB fusion of *C. pneumonia*

SEQ ID NO: 44 is a first determined DNA sequence for the *C. trachomatis* LGV II clone 19783.3.jen.seq(1>509)CTL2#11-3', representing the 3' end.

SEQ ID NO: 45 is a second determined DNA sequence for the *C. trachomatis* LGV II clone 19783.4.jen.seq(1>481)CTL2#11-5', representing the 5' end.

SEQ ID NO: 46 is the determined DNA sequence for the C. trachomatis LGV II clone 19784CTL2\_12consensus.seq(1>427)CTL2#12.

SEQ ID NO: 47 is the determined DNA sequence for the C. trachomatis LGV II clone 19785.4.jen.seq(1>600)CTL2#16-5', representing the 5' end.

SEQ ID NO: 48 is a first determined DNA sequence for the C. trachomatis LGV II clone 19786.3.jen.seq(1>600)CTL2#18-3', representing the 3' end.

SEQ ID NO: 49 is a second determined DNA sequence for the C. trachomatis LGV II clone 19786.4.jen.seq(1>600)CTL2#18-5', representing the 5' end.

SEQ ID NO: 50 is the determined DNA sequence for the C. trachomatis LGV II clone 19788CTL2\_21consensus.seq(1>406)CTL2#21.

SEQ ID NO: 51 is the determined DNA sequence for the C. trachomatis LGV II clone 19790CTL2\_23consensus.seq(1>602)CTL2#23.

SEQ ID NO: 52 is the determined DNA sequence for the C. trachomatis LGV II clone 19791CTL2\_24consensus.seq(1>145)CTL2#24.

SEQ ID NO: 53 is the determined DNA sequence for the C. trachomatis LGV II clone CTL2#4.

SEQ ID NO: 54 is the determined DNA sequence for the C. trachomatis LGV II clone CTL2#8b.

SEQ ID NO: 55 is the determined DNA sequence for the C. trachomatis LGV II clone 15-G1-89, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 56 is the determined DNA sequence for the C. trachomatis LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 57 is the determined DNA sequence for the C. trachomatis LGV II clone 12-G3-83, sharing homology to the hypothetical protein CT622.

SEQ ID NO: 58 is the determined DNA sequence for the C. trachomatis LGV II clone 12-B3-95, sharing homology to the lipoamide dehydrogenase gene CT557.

SEQ ID NO: 59 is the determined DNA sequence for the C. trachomatis LGV II clone 11-H4-28, sharing homology to the dnaK gene CT396.

SEQ ID NO: 60 is the determined DNA sequence for the C. trachomatis LGV II clone 11-H3-68, sharing partial homology to the PGP6-D virulence protein and L1 ribosomal gene CT318.

SEQ ID NO: 61 is the determined DNA sequence for the C. trachomatis LGV II clone 11-G1-34, sharing partial homology to the malate dehydrogenase gene CT376 and to the glycogen hydrolase gene CT042.

SEQ ID NO: 62 is the determined DNA sequence for the C. trachomatis LGV II clone 11-G10-46, sharing homology to the hypothetical protein CT610.

SEQ ID NO: 63 is the determined DNA sequence for the C. trachomatis LGV II clone 11-C12-91, sharing homology to the OMP2 gene CT443.

SEQ ID NO: 64 is the determined DNA sequence for the C. trachomatis LGV II clone 11-A3-93, sharing homology to the HAD superfamily gene CT103.

SEQ ID NO: 65 is the determined amino acid sequence for the C. trachomatis LGV II clone 14-H1-4, sharing homology to the thiol specific antioxidant gene CT603.

SEQ ID NO: 66 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#9.

SEQ ID NO: 67 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#7.

SEQ ID NO: 68 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#6.

SEQ ID NO: 69 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#5.

SEQ ID NO: 70 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#2.

SEQ ID NO: 71 is the determined DNA sequence for the C. trachomatis LGV II clone CtL2#1.

SEQ ID NO: 72 is a first determined DNA sequence for the C. trachomatis LGV II clone 23509.2CtL2#3-5', representing the 5' end.

SEQ ID NO: 73 is a second determined DNA sequence for the C. trachomatis LGV II clone 23509.1CtL2#3-3', representing the 3' end.

SEQ ID NO: 74 is a first determined DNA sequence for the C. trachomatis LGV II clone 22121.2CtL2#10-5', representing the 5' end.

SEQ ID NO: 75 is a second determined DNA sequence for the C. trachomatis LGV II clone 22121.1CtL2#10-3', representing the 3' end.

SEQ ID NO: 76 is the determined DNA sequence for the C. trachomatis LGV II clone 19787.6CtL2#19-5', representing the 5' end.

SEQ ID NO: 77 is the determined DNA sequence for the C. pneumoniae LGV II clone CpS13-His.

SEQ ID NO: 78 is the determined DNA sequence for the C. pneumoniae LGV II clone Cp\_SWIB-His.

SEQ ID NO: 79 is the determined DNA sequence for the C. trachomatis LGV II clone 23-G7-68, sharing partial homology to the L11, L10 and L1 ribosomal protein.

SEQ ID NO: 80 is the determined DNA sequence for the C. trachomatis LGV II clone 22-F8-91, sharing homology to the pmpC gene.

SEQ ID NO: 81 is the determined DNA sequence for the C. trachomatis LGV II clone 21-E8-95, sharing homology to the CT610-CT613 genes.

SEQ ID NO: 82 is the determined DNA sequence for the C. trachomatis LGV II clone 19-F12-57, sharing homology to the CT858 and recA genes.

SEQ ID NO: 83 is the determined DNA sequence for the C. trachomatis LGV II clone 19-F12-53, sharing homology to the CT445 gene encoding glutamyl tRNA synthetase.

SEQ ID NO: 84 is the determined DNA sequence for the C. trachomatis LGV II clone 19-A5-54, sharing homology to the cryptic plasmid gene.

SEQ ID NO: 85 is the determined DNA sequence for the C. trachomatis LGV II clone 17-E11-72, sharing partial homology to the OppC\_2 and pmpD genes.

SEQ ID NO: 86 is the determined DNA sequence for the C. trachomatis LGV II clone 17-C1-77, sharing partial homology to the CT857 and CT858 open reading frames.

SEQ ID NO: 87 is the determined DNA sequence for the C. trachomatis LGV II clone 15-H2-76, sharing partial homology to the pmpD and SycE genes, and to the CT089 ORF.

SEQ ID NO: 88 is the determined DNA sequence for the *C. trachomatis* LGV II clone 15-A3-26, sharing homology to the CT858 ORF.

SEQ ID NO: 89 is the determined amino acid sequence for the *C. pneumoniae* clone Cp\_SWIB-His.

SEQ ID NO: 90 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2\_LPDA\_FL.

SEQ ID NO: 91 is the determined amino acid sequence for the *C. pneumoniae* clone CpS13-His.

SEQ ID NO: 92 is the determined amino acid sequence for the *C. trachomatis* LGV II clone CtL2\_TSA\_FL.

SEQ ID NO: 93 is the amino acid sequence for Ct-Swib 43-61 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 94 is the amino acid sequence for Ct-Swib 48-67 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 95 is the amino acid sequence for Ct-Swib 52-71 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 96 is the amino acid sequence for Ct-Swib 58-77 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 97 is the amino acid sequence for Ct-Swib 63-82 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 98 is the amino acid sequence for Ct-Swib 51-66 peptide from *C. trachomatis* LGV II.

SEQ ID NO: 99 is the amino acid sequence for Cp-Swib 52-67 peptide from *C. pneumonia*.

SEQ ID NO: 100 is the amino acid sequence for Cp-Swib 37-51 peptide from *C. pneumonia*.

SEQ ID NO: 101 is the amino acid sequence for Cp-Swib 32-51 peptide from *C. pneumonia*.

SEQ ID NO: 102 is the amino acid sequence for Cp-Swib 37-56 peptide from *C. pneumonia*.

SEQ ID NO: 103 is the amino acid sequence for Ct-Swib 36-50 peptide from *C. trachomatis*.

SEQ ID NO: 104 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 105 is the amino acid sequence for Ct-S13 60-80 peptide from *C. trachomatis*.

SEQ ID NO: 106 is the amino acid sequence for Ct-S13 1-20 peptide from *C. trachomatis*.

SEQ ID NO: 107 is the amino acid sequence for Ct-S13 46-65 peptide from *C. trachomatis*.

SEQ ID NO: 108 is the amino acid sequence for Ct-S13 56-75 peptide from *C. trachomatis*.

SEQ ID NO: 109 is the amino acid sequence for Cp-S13 56-75 peptide from *C. pneumoniae*.

SEQ ID NO: 110 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-G12-60, containing partial open reading frames for hypothetical proteins CT875, CT229 and CT228.

SEQ ID NO: 111 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-B3-53, sharing homology to the CT110 ORF of GroEL.

SEQ ID NO: 112 is the determined DNA sequence for the *C. trachomatis* LGV II clone 22-A1-49, sharing partial homology to the CT660 and CT659 ORFs.

SEQ ID NO: 113 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-E2-9, sharing partial homology to the CT611 and CT 610 ORFs.

SEQ ID NO: 114 is the determined DNA sequence for the *C. trachomatis* LGV II clone 17-C10-31, sharing partial homology to the CT858 ORF.

SEQ ID NO: 115 is the determined DNA sequence for the *C. trachomatis* LGV II clone 21-C7-66, sharing homology to the dnaK-like gene.

SEQ ID NO: 116 is the determined DNA sequence for the *C. trachomatis* LGV II clone 20-G3-45, containing part of the pmpB gene CT413.

SEQ ID NO: 117 is the determined DNA sequence for the *C. trachomatis LGV II* clone 18-C5-2, sharing homology to the S1 ribosomal protein ORF.

SEQ ID NO: 118 is the determined DNA sequence for the *C. trachomatis LGV II* clone 17-C5-19, containing part of the ORFs for CT431 and CT430.

SEQ ID NO: 119 is the determined DNA sequence for the *C. trachomatis LGV II* clone 16-D4-22, contains partial sequences of ORF3 and ORF4 of the plasmid for growth within mammalian cells.

SEQ ID NO: 120 is the determined full-length DNA sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 121 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar LGV II Cap1 gene CT529.

SEQ ID NO: 122 is the determined full-length DNA sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 123 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar E Cap1 gene CT529.

SEQ ID NO: 124 is the determined full-length DNA sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 125 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar 1A Cap1 gene CT529.

SEQ ID NO: 126 is the determined full-length DNA sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 127 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar G Cap1 gene CT529.

SEQ ID NO: 128 is the determined full-length DNA sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 129 is the predicted full-length amino acid sequence for the *C. trachomatis* serovar F1 NII Cap1 gene CT529.

SEQ ID NO: 130 is the determined full-length DNA sequence for the *C. trachomatis* serovar L1 Cap1 gene CT529.

SEQ ID NO: 131 is the predicted full-length amino acid sequence for the C. trachomatis serovar L1 Cap1 gene CT529.

SEQ ID NO: 132 is the determined full-length DNA sequence for the C. trachomatis serovar L3 Cap1 gene CT529.

SEQ ID NO: 133 is the predicted full-length amino acid sequence for the C. trachomatis serovar L3 Cap1 gene CT529.

SEQ ID NO: 134 is the determined full-length DNA sequence for the C. trachomatis serovar Ba Cap1 gene CT529.

SEQ ID NO: 135 is the predicted full-length amino acid sequence for the C. trachomatis serovar Ba Cap1 gene CT529.

SEQ ID NO: 136 is the determined full-length DNA sequence for the C. trachomatis serovar MOPN Cap1 gene CT529.

SEQ ID NO: 137 is the predicted full-length amino acid sequence for the C. trachomatis serovar MOPN Cap1 gene CT529.

SEQ ID NO: 138 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #124-139 of *C. trachomatis* serovar L2.

SEQ ID NO: 139 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #132-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 140 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-155 of *C. trachomatis* serovar L2.

SEQ ID NO: 141 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #146-163 of *C. trachomatis* serovar L2.

SEQ ID NO: 142 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #154-171 of *C. trachomatis* serovar L2.

SEQ ID NO: 143 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #162-178 of *C. trachomatis* serovar L2.

SEQ ID NO: 144 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 145 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #139-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 146 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #140-147 of *C. trachomatis* serovar L2.

SEQ ID NO: 147 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-146 of *C. trachomatis* serovar L2.

SEQ ID NO: 148 is the determined amino acid sequence for the Cap1 CT529 ORF peptide #138-145 of *C. trachomatis* serovar L2.

SEQ ID NO: 149 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # F140->I of *C. trachomatis* serovar L2.

SEQ ID NO: 150 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Ga of *C. trachomatis* serovar L2.

SEQ ID NO: 151 is the determined amino acid sequence for the Cap1 CT529 ORF peptide # #S139>Gb of *C. trachomatis* serovar L2.

SEQ ID NO: 152 is the determined amino acid sequence for the peptide # 2 C7.8-6 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 153 is the determined amino acid sequence for the peptide # 2 C7.8-7 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 154 is the determined amino acid sequence for the peptide # 2 C7.8-8 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 155 is the determined amino acid sequence for the peptide # 2 C7.8-9 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 156 is the determined amino acid sequence for the peptide # 2 C7.8-10 of the 216aa ORF of *C. trachomatis* serovar L2.

SEQ ID NO: 157 is the determined amino acid sequence for the 53 amino acid residue peptide of the 216aa ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 158 is the determined amino acid sequence for the 52 amino acid residue peptide of the CT529 ORF within clone 2C7.8 of *C. trachomatis* serovar L2.

SEQ ID NO: 159 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 160 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar L2.

SEQ ID NO: 161 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 for serovars other than L2 and MOPN.

SEQ ID NO: 162 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovars other than L2 and MOPN.

SEQ ID NO: 163 is the determined DNA sequence for the 5' (forward) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 164 is the determined DNA sequence for the 5' (reverse) primer for cloning full-length CT529 serovar MOPN.

SEQ ID NO: 165 is the determined DNA sequence for the 5' (forward) primer for pBIB-KS.

SEQ ID NO: 166 is the determined DNA sequence for the 5' (reverse) primer for pBIB-KS.

SEQ ID NO: 167 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar L2.

SEQ ID NO: 168 is the determined amino acid sequence for the 9-mer epitope peptide Cap1#139-147 from serovar D.

SEQ ID NO: 169 is the determined full-length DNA sequence for the *C. trachomatis* pmpI gene.

SEQ ID NO: 170 is the determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 171 is the determined full-length DNA sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 172 is the determined full-length DNA sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 173 is the determined full-length DNA sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 174 is the determined full-length DNA sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 175 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpl gene.

SEQ ID NO: 176 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 177 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 178 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 179 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 180 is the predicted full-length amino acid sequence for the *C. trachomatis* pmpB gene.

SEQ ID NO: 181 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpl gene.

SEQ ID NO: 182 is a subsequently determined full-length DNA sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 183 is the determined DNA sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 184 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 185 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 186 is a first determined DNA sequence representing the carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 187 is a second determined DNA sequence representing the amino terminus minus the signal sequence for the *C. trachomatis* pmpC gene.

SEQ ID NO: 188 is the determined DNA sequence representing the *C. pneumoniae* serovar MOMPS pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 189 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpl gene.

SEQ ID NO: 190 is subsequently predicted amino acid sequence for the *C. trachomatis* pmpG gene.

SEQ ID NO: 191 is the predicted amino acid sequence minus the signal sequence for the *C. trachomatis* pmpE gene.

SEQ ID NO: 192 is a first predicted amino acid sequence representing the carboxy terminus for the *C. trachomatis* pmpD gene.

SEQ ID NO: 193 is a second predicted amino acid sequence representing the Amino terminus minus the signal sequence for the *C. trachomatis* pmpD gene.

SEQ ID NO: 194 is a first predicted amino acid sequence representing the Carboxy terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 195 is a second predicted amino acid sequence representing the Amino terminus for the *C. trachomatis* pmpC gene.

SEQ ID NO: 196 is the predicted amino acid sequence representing the *C. pneumoniae* serovar MOMP pmp gene in a fusion molecule with Ra12.

SEQ ID NO: 197 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 198 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 199 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpC gene in the SKB vaccine vector.

SEQ ID NO: 200 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 201 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 202 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpD gene in the SKB vaccine vector.

SEQ ID NO: 203 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 204 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the SKB vaccine vector.

SEQ ID NO: 205 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 206 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

SEQ ID NO: 207 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 208 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 209 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 210 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpC gene in the pET17b vector.

SEQ ID NO: 211 is the determined DNA sequence for the 5' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 212 is the determined DNA sequence for the 3' oligo primer for cloning the amino terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 213 is the determined DNA sequence for the 5' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 214 is the determined DNA sequence for the 3' oligo primer for cloning the carboxy terminus portion of the *C. trachomatis* pmpD gene in the pET17b vector.

SEQ ID NO: 215 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 216 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 217 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 218 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpE gene in the pET17b vector.

SEQ ID NO: 219 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 220 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 221 is the amino acid sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the pET17b vector.

SEQ ID NO: 222 is the determined DNA sequence for the 5' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 223 is the determined DNA sequence for the 3' oligo primer for cloning the *C. trachomatis* pmpI gene in the pET17b vector.

SEQ ID NO: 224 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 1-20.

SEQ ID NO: 225 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 6-25.

SEQ ID NO: 226 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 12-31.

SEQ ID NO: 227 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 17-36.

SEQ ID NO: 228 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 22-41.

SEQ ID NO: 229 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 27-46.

SEQ ID NO: 230 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 42-61.

SEQ ID NO: 231 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 46-65.

SEQ ID NO: 232 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 51-70.

SEQ ID NO: 233 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 56-75.

SEQ ID NO: 234 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 61-80.

SEQ ID NO: 235 is the determined amino acid sequence for the *C. pneumoniae* Swib peptide 66-87.

SEQ ID NO: 236 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 103-122.

SEQ ID NO: 237 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 108-127.

SEQ ID NO: 238 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 113-132.

SEQ ID NO: 239 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 118-137.

SEQ ID NO: 240 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 123-143.

SEQ ID NO: 241 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 128-147.

SEQ ID NO: 242 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 133-152.

SEQ ID NO: 243 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 137-156.

SEQ ID NO: 244 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 142-161.

SEQ ID NO: 245 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 147-166.

SEQ ID NO: 246 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 152-171.

SEQ ID NO: 247 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 157-176.

SEQ ID NO: 248 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 162-181.

SEQ ID NO: 249 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 167-186.

SEQ ID NO: 250 is the determined amino acid sequence for the *C. trachomatis* OMCB peptide 171-190.

SEQ ID NO: 251 is the determined amino acid sequence for the *C. trachomatis* OMBC peptide 171-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMBC peptide 175-186.

SEQ ID NO: 252 is the determined amino acid sequence for the *C. trachomatis* OMBC peptide 175-186.

SEQ ID NO: 253 is the determined amino acid sequence for the *C. pneumoniae* OMBC peptide 185-198.

SEQ ID NO: 254 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 96-115.

SEQ ID NO: 255 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 101-120.

SEQ ID NO: 256 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 106-125.

SEQ ID NO: 257 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 111-130.

SEQ ID NO: 258 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 116-135.

SEQ ID NO: 259 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 121-140.

SEQ ID NO: 260 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 126-145.

SEQ ID NO: 261 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 131-150.

SEQ ID NO: 262 is the determined amino acid sequence for the *C. trachomatis* TSA peptide 136-155.

SEQ ID NO: 263 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 264 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar I.

SEQ ID NO: 265 is the determined full-length DNA sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 266 is the predicted full-length amino sequence for the *C. trachomatis* CT529/Cap 1 gene serovar K.

SEQ ID NO: 267 is the determined DNA sequence for the *C. trachomatis* clone 17-G4-36 sharing homology to part of the ORF of DNA-directed RNA polymerase beta subunit- CT315 in serD.

SEQ ID NO: 268 is the determined DNA sequence for the partial sequence of the *C. trachomatis* CT016 gene in clone 2E10.

SEQ ID NO: 269 is the determined DNA sequence for the partial sequence of the *C. trachomatis* tRNA syntase gene in clone 2E10.

SEQ ID NO: 270 is the determined DNA sequence for the partial sequence for the *C. trachomatis* clpX gene in clone 2E10.

SEQ ID NO: 271 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 5'end.

SEQ ID NO: 272 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-30 representing the 3'end.

SEQ ID NO: 273 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-28.

SEQ ID NO: 274 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-27.

SEQ ID NO: 275 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-26.

SEQ ID NO: 276 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-24.

SEQ ID NO: 277 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-23.

SEQ ID NO: 278 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-21.

SEQ ID NO: 279 is the determined DNA sequence for the *C. trachomatis*

clone CtL2gam-18.

SEQ ID NO: 280 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-17.

SEQ ID NO: 281 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 5' end.

SEQ ID NO: 282 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-15 representing the 3' end.

SEQ ID NO: 283 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-13.

SEQ ID NO: 284 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-10.

SEQ ID NO: 285 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-8.

SEQ ID NO: 286 is a first determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 5' end.

SEQ ID NO: 287 is a second determined DNA sequence for the *C. trachomatis* clone CtL2gam-6 representing the 3' end.

SEQ ID NO: 288 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-5.

SEQ ID NO: 289 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-2.

SEQ ID NO: 290 is the determined DNA sequence for the *C. trachomatis* clone CtL2gam-1.

SEQ ID NO: 291 is the determined full-length DNA sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 292 is the predicted full-length amino acid sequence for the *C. pneumoniae* homologue of the CT529 gene.

SEQ ID NO: 293 is the determined DNA sequence for the insertion sequence for cloning the *C. trachomatis* pmpG gene in the SKB vaccine vector.

**DESCRIPTION OF THE FIGURES**

Fig. 1 illustrates induction of INF- $\gamma$  from a *Chlamydia*-specific T cell line activated by target cells expressing clone 4C9-18#2.

Fig. 2 illustrates retroviral vectors pBIB-KS1,2,3 modified to contain a Kosak translation initiation site and stop codons.

Fig. 3 shows specific lysis in a chromium release assay of P815 cells pulsed with *Chlamydia* peptides CtC7.8-12 (SEQ ID NO: 18) and CtC7.8-13 (SEQ ID NO: 19).

Fig. 4 shows antibody isotype titers in C57Bl/6 mice immunized with *C. trachomatis* SWIB protein.

Fig. 5 shows *Chlamydia*-specific T-cell proliferative responses in splenocytes from C3H mice immunized with *C. trachomatis* SWIB protein.

Fig. 6 illustrates the 5' and 3' primer sequences designed from *C. pneumoniae* which were used to isolate the SWIB and S13 genes from *C. pneumoniae*.

Figs. 7A and 7B show induction of IFN- $\gamma$  from a human anti-*chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* upon activation by monocyte-derived dendritic cells expressing chlamydial proteins.

Fig. 8 shows the identification of T cell epitopes in Chlamydial ribosomal S13 protein with T-cell line TCL 8 EB/DC.

Fig. 9 illustrates the proliferative response of CP-21 T-cells generated against *C. pneumoniae*-infected dendritic cells to recombinant *C. pneumonia*-SWIBprotein, but not *C. trachomatis* SWIB protein.

Fig. 10 shows the *C. trachomatis*-specific SWIB proliferative responses of a primary T-cell line (TCT-10 EB) from an asymptomatic donor.

Fig. 11 illustrates the identification of T-cell epitope in *C. trachomatis* SWIB with an antigen specific T-cell line (TCL-10 EB).

## DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the diagnosis and treatment of Chlamydial infection. In one aspect, the compositions of the subject invention include polypeptides that comprise at least one immunogenic portion of a *Chlamydia* antigen, or a variant thereof.

In specific embodiments, the subject invention discloses polypeptides comprising an immunogenic portion of a *Chlamydia* antigen, wherein the *Chlamydia* antigen comprises an amino acid sequence encoded by a polynucleotide molecule including a sequence selected from the group consisting of (a) nucleotide sequences recited in SEQ ID NO: 1, 15, 21-25, 44-64, 66-76, 79-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-290 (b) the complements of said nucleotide sequences, and (c) variants of such sequences.

As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the inventive antigens may consist entirely of the immunogenic portion, or may contain additional sequences. The additional sequences may be derived from the native *Chlamydia* antigen or may be heterologous, and such sequences may (but need not) be immunogenic.

The term "polynucleotide(s)," as used herein, means a single or double-stranded polymer of deoxyribonucleotide or ribonucleotide bases and includes DNA and corresponding RNA molecules, including HnRNA and mRNA molecules, both sense and anti-sense strands, and comprehends cDNA, genomic DNA and recombinant DNA, as well as wholly or partially synthesized polynucleotides. An HnRNA molecule contains introns and corresponds to a DNA molecule in a generally one-to-one manner. An mRNA molecule corresponds to an HnRNA and DNA molecule from which the introns have been excised. A polynucleotide may consist of an entire gene, or any portion thereof. Operable anti-sense polynucleotides may comprise a fragment of the corresponding polynucleotide, and the definition of "polynucleotide" therefore includes all such operable anti-sense fragments.

An "immunogenic portion" of an antigen is a portion that is capable of reacting with sera obtained from a *Chlamydia*-infected individual (*i.e.*, generates an absorbance reading with sera from infected individuals that is at least three standard deviations above the absorbance obtained with sera from uninfected individuals, in a representative ELISA assay described herein). Such immunogenic portions generally comprise at least about 5 amino acid residues, more preferably at least about 10, and most

preferably at least about 20 amino acid residues. Methods for preparing and identifying immunogenic portions of antigens of known sequence are well known in the art and include those summarized in Paul, *Fundamental Immunology*, 3<sup>rd</sup> ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptides for the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and antibodies may be prepared as described herein, and using well known techniques. An immunogenic portion of a native *Chlamydia* protein is a portion that reacts with such antisera and/or T-cells at a level that is not substantially less than the reactivity of the full length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Such immunogenic portions may react within such assays at a level that is similar to or greater than the reactivity of the full length polypeptide. Such screens may generally be performed using methods well known to those of ordinary skill in the art, such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. For example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

Examples of immunogenic portions of antigens contemplated by the present invention include, for example, the T cell stimulating epitopes provided in SEQ ID NO: 9, 10, 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256. Polypeptides comprising at least an immunogenic portion of one or more *Chlamydia* antigens as described herein may generally be used, alone or in combination, to detect Chlamydial infection in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and polynucleotide molecules. Such variants include, but are not limited to, naturally occurring allelic variants of the inventive sequences. In particular, variants include other *Chlamydiae* serovars, such as serovars D, E and F, as well as the several LGV serovars which share homology to the inventive polypeptide and

polynucleotide molecules described herein. Preferably, the serovar homologues show 95-99% homology to the corresponding polypeptide sequence(s) described herein.

A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are retained. In a preferred embodiment, variant polypeptides differ from an identified sequence by substitution, deletion or addition of five amino acids or fewer. Such variants may generally be identified by modifying one of the above polypeptide sequences, and evaluating the antigenic properties of the modified polypeptide using, for example, the representative procedures described herein. In other words, the ability of a variant to react with antigen-specific antisera may be enhanced or unchanged, relative to the native protein, or may be diminished by less than 50%, and preferably less than 20%, relative to the native protein. Such variants may generally be identified by modifying one of the above polypeptide sequences and evaluating the reactivity of the modified polypeptide with antigen-specific antibodies or antisera as described herein. Preferred variants include those in which one or more portions, such as an N-terminal leader sequence or transmembrane domain, have been removed. Other preferred variants include variants in which a small portion (e.g., 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity (determined as described below) to the identified polypeptides.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. Amino acid substitutions may generally be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may represent

conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydropathic nature of the polypeptide. Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A polynucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions such that the immunogenicity of the encoded polypeptide is not diminished, relative to the native protein. The effect on the immunogenicity of the encoded polypeptide may generally be assessed as described herein. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants as discussed below, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity (determined as described below) to the recited sequence.

The polypeptides provided by the present invention include variants that are encoded by polynucleotide sequences which are substantially homologous to one or more of the polynucleotide sequences specifically recited herein. "Substantial homology," as used herein, refers to polynucleotide sequences that are capable of hybridizing under moderately

stringent conditions. Suitable moderately stringent conditions include prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the event of cross-species homology, at 45°C with 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. Such hybridizing polynucleotide sequences are also within the scope of this invention, as are nucleotide sequences that, due to code degeneracy, encode a polypeptide that is the same as a polypeptide of the present invention.

Two nucleotide or polypeptide sequences are said to be "identical" if the sequence of nucleotides or amino acid residues in the two sequences is the same when aligned for maximum correspondence as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) Fast and sensitive multiple sequence alignments on a microcomputer *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) Optimal alignments in linear space *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) The neighbor joining method. A new method for reconstructing phylogenetic trees *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San

Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) Rapid similarity searches of nucleic acid and protein data banks *Proc. Natl. Acad., Sci. USA* 80:726-730.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (i.e. gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (i.e. the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

Also included in the scope of the present invention are alleles of the genes encoding the nucleotide sequences recited in herein. As used herein, an "allele" or "allelic sequence" is an alternative form of the gene which may result from at least one mutation in the nucleic acid sequence. Alleles may result in altered mRNAs or polypeptides whose structure or function may or may not be altered. Any given gene may have none, one, or many allelic forms. Common mutational changes which give rise to alleles are generally ascribed to natural deletions, additions, or substitutions of nucleotides. Each of these types of changes may occur alone or in combination with the others, one or more times in a given sequence. In specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *Chlamydia* antigen (or a variant of such an antigen), that comprises one or more of the amino acid sequences encoded by (a) a polynucleotide sequence selected from the group consisting of SEQ ID NO: 1-4, 15 21-25, 44-64, 66-76 and 79-88; (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b). As discussed in the Examples below, several of the *Chlamydia* antigens disclosed herein recognize a T cell line that recognizes both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, indicating that they may represent an immunoreactive epitope shared by *Chlamydia trachomatis* and

*Chlamydia pneumoniae*. The antigens may thus be employed in a vaccine for both *C. trachomatis* genital tract infections and for *C. pneumonia* infections. Further characterization of these *Chlamydia* antigens from *Chlamydia trachomatis* and *Chlamydia pneumonia* to determine the extent of cross-reactivity is provided in Example 6. Additionally, Example 4 describes cDNA fragments (SEQ ID NO: 15, 16 and 33) isolated from *C. trachomatis* which encode proteins (SEQ ID NO: 17-19 and 32) capable of stimulating a *Chlamydia*-specific murine CD8+ T cell line.

In general, *Chlamydia* antigens, and polynucleotide sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, polynucleotide molecules encoding *Chlamydia* antigens may be isolated from a *Chlamydia* genomic or cDNA expression library by screening with a *Chlamydia*-specific T cell line as described below, and sequenced using techniques well known to those of skill in the art. Additionally, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for *Chlamydia*-associated expression (*i.e.*, expression that is at least two fold greater in *Chlamydia*-infected cells than in controls, as determined using a representative assay provided herein). Such screens may be performed using a Synteni microarray (Palo Alto, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polypeptides may be amplified from cDNA prepared from cells expressing the proteins described herein.. Such polynucleotides may be amplified via polymerase chain reaction (PCR). For this approach, sequence-specific primers may be designed based on the sequences provided herein, and may be purchased or synthesized.

Antigens may be produced recombinantly, as described below, by inserting a polynucleotide sequence that encodes the antigen into an expression vector and expressing the antigen in an appropriate host. Antigens may be evaluated for a desired property, such as the ability to react with sera obtained from a *Chlamydia*-infected individual as described herein, and may be sequenced using, for example, traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

Polynucleotide sequences encoding antigens may also be obtained by screening an appropriate *Chlamydia* cDNA or genomic DNA library for polynucleotide sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY (and references cited therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a cDNA or genomic library. The library screen may then be performed using the isolated probe.

An amplified portion may be used to isolate a full length gene from a suitable library (e.g., a *Chlamydia* cDNA library) using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes. Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (e.g., by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe (see Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences are then assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known

techniques.

Alternatively, there are numerous amplification techniques for obtaining a full length coding sequence from a partial cDNA sequence. Within such techniques, amplification is generally performed via PCR. Any of a variety of commercially available kits may be used to perform the amplification step. Primers may be designed using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.* 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989), and software well known in the art may also be employed. Primers are preferably 22-30 nucleotides in length, have a GC content of at least 50% and anneal to the target sequence at temperatures of about 68°C to 72°C. The amplified region may be sequenced as described above, and overlapping sequences assembled into a contiguous sequence.

One such amplification technique is inverse PCR (see Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic.* 1:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res.* 19:3055-60, 1991). Transcription-Mediated Amplification, or TMA is another method that may be utilized for the amplification of DNA, rRNA, or mRNA, as described in Patent No. PCT/US91/03184. This autocatalytic and isothermal non-PCR based method utilizes two primers and two enzymes: RNA polymerase and reverse transcriptase. One primer contains a promoter sequence for RNA polymerase. In the first amplification, the promoter-primer hybridizes to the target rRNA at a defined site. Reverse transcriptase creates a DNA copy of the target rRNA by extension from the 3' end of the promoter-primer. The RNA in the resulting complex is degraded and a second primer binds to the DNA copy. A

new strand of DNA is synthesized from the end of the primer by reverse transcriptase creating double stranded DNA. RNA polymerase recognizes the promoter sequence in the DNA template and initiates transcription. Each of the newly synthesized RNA amplicons re-enters the TMA process and serves as a template for a new round of replication leading to the exponential expansion of the RNA amplicon. Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (*e.g.*, NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length cDNA sequences may also be obtained by analysis of genomic fragments.

Polynucleotide variants may generally be prepared by any method known in the art, including chemical synthesis by, for example, solid phase phosphoramidite chemical synthesis. Modifications in a polynucleotide sequence may also be introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis (*see* Adelman et al., *DNA* 2:183, 1983). Alternatively, RNA molecules may be generated by *in vitro* or *in vivo* transcription of DNA sequences encoding a *Chlamydial* protein, or portion thereof, provided that the DNA is incorporated into a vector with a suitable RNA polymerase promoter (such as T7 or SP6). Certain portions may be used to prepare an encoded polypeptide, as described herein. In addition, or alternatively, a portion may be administered to a patient such that the encoded polypeptide is generated *in vivo* (*e.g.*, by transfecting antigen-presenting cells, such as dendritic cells, with a cDNA construct encoding a *Chlamydial* polypeptide, and administering the transfected cells to the patient).

A portion of a sequence complementary to a coding sequence (*i.e.*, an antisense polynucleotide) may also be used as a probe or to modulate gene expression. cDNA constructs that can be transcribed into antisense RNA may also be introduced into cells of tissues to facilitate the production of antisense RNA. An antisense polynucleotide may be used, as described herein, to inhibit expression of a *Chlamydial* protein. Antisense technology can be used to control gene expression through triple-helix formation, which

compromises the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors or regulatory molecules (see Gee et al., *In Huber and Carr, Molecular and Immunologic Approaches*, Futura Publishing Co. (Mt. Kisco, NY; 1994)). Alternatively, an antisense molecule may be designed to hybridize with a control region of a gene (e.g., promoter, enhancer or transcription initiation site), and block transcription of the gene; or to block translation by inhibiting binding of a transcript to ribosomes.

A portion of a coding sequence, or of a complementary sequence, may also be designed as a probe or primer to detect gene expression. Probes may be labeled with a variety of reporter groups, such as radionuclides and enzymes, and are preferably at least 10 nucleotides in length, more preferably at least 20 nucleotides in length and still more preferably at least 30 nucleotides in length. Primers, as noted above, are preferably 22-30 nucleotides in length.

Any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of nontraditional bases such as inosine, queosine and wybutoxine, as well as acetyl-, methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Nucleotide sequences as described herein may be joined to a variety of other nucleotide sequences using established recombinant DNA techniques. For example, a polynucleotide may be cloned into any of a variety of cloning vectors, including plasmids, phagemids, lambda phage derivatives and cosmids. Vectors of particular interest include expression vectors, replication vectors, probe generation vectors and sequencing vectors. In general, a vector will contain an origin of replication functional in at least one organism, convenient restriction endonuclease sites and one or more selectable markers. Other elements will depend upon the desired use, and will be apparent to those of ordinary skill in the art.

Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where

amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division, Foster City, CA, and may be operated according to the manufacturer's instructions.

As noted above, immunogenic portions of *Chlamydia* antigens may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen for immunogenic properties. The representative ELISAs described herein may generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates a signal in such assays that is substantially similar to that generated by the full length antigen. In other words, an immunogenic portion of a *Chlamydia* antigen generates at least about 20%, and preferably about 100%, of the signal induced by the full length antigen in a model ELISA as described herein.

Portions and other variants of *Chlamydia* antigens may be generated by synthetic or recombinant means. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the polynucleotide sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a polynucleotide sequence encoding the polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides as described herein. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an

expression vector containing a polynucleotide molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in an isolated, substantially pure, form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most preferably at least about 99% pure.

Within certain specific embodiments, a polypeptide may be a fusion protein that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known *Chlamydial* protein. A fusion partner may, for example, assist in providing T helper epitopes (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the protein or to enable the protein to be targeted to desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the protein. A DNA sequence encoding a fusion protein of the present invention may be constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding, for example, the first and second polypeptides, into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the

fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8562, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. As an alternative to the use of a peptide linker sequence (when desired), one can utilize non-essential N-terminal amino acid regions (when present) on the first and second polypeptides to separate the functional domains and prevent steric hindrance.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Fusion proteins are also provided that comprise a polypeptide of the present invention together with an unrelated immunogenic protein. Preferably the immunogenic protein is capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (see, for example, Stoute et al. *New Engl. J. Med.*, 336:86-91, 1997).

Within preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenzae* B (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (e.g., the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as

an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1 (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine amidase known as amidase LYTA (encoded by the LytA gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (see *Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion protein. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305. Additionally, the fusion protein Ra12 may be linked to the inventive polynucleotides to facilitate protein expression.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or polynucleotides encoding such polypeptides or fusion proteins) to induce protective immunity against Chlamydial infection in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat Chlamydial infection.

In this aspect, the polypeptide, fusion protein or polynucleotide molecule is generally present within a pharmaceutical composition or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and an immunostimulant,

such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical compositions and vaccines may also contain other *Chlamydia* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain polynucleotides encoding one or more polypeptides or fusion proteins as described above, such that the polypeptide is generated *in situ*. In such vaccines, the polynucleotides may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary polynucleotide sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface. In a preferred embodiment, the polynucleotides may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective) virus. Techniques for incorporating polynucleotides into such expression systems are well known to those of ordinary skill in the art. The polynucleotides may also be administered as "naked" plasmid vectors as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. Techniques for incorporating DNA into such vectors are well known to those of ordinary skill in the art. A retroviral vector may additionally transfer or incorporate a gene for a selectable marker (to aid in the identification or selection of transduced cells) and/or a targeting moiety, such as a gene that encodes a ligand for a receptor on a specific target cell, to render the vector target specific. Targeting may also be accomplished using an antibody, by methods known to those of ordinary skill in the art.

Other formulations for therapeutic purposes include colloidal dispersion systems, such as macromolecule complexes, nanocapsules, microspheres, beads, and lipid-based systems including oil-in-water emulsions, micelles, mixed micelles, and liposomes. A preferred colloidal system for use as a delivery vehicle *in vitro* and *in vivo* is a liposome (*i.e.*, an artificial membrane vesicle). The uptake of naked polynucleotides may be increased by incorporating the polynucleotides into and/or onto biodegradable beads, which are efficiently transported into the cells. The preparation and use of such systems is well known in the art.

In a related aspect, a polynucleotide vaccine as described above may be administered simultaneously with or sequentially to either a polypeptide of the present invention or a known *Chlamydia* antigen. For example, administration of polynucleotides encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the vaccine.

Polypeptides and polynucleotides disclosed herein may also be employed in adoptive immunotherapy for the treatment of *Chlamydial* infection. Adoptive immunotherapy may be broadly classified into either active or passive immunotherapy. In active immunotherapy, treatment relies on the *in vivo* stimulation of the endogenous host immune system with the administration of immune response-modifying agents (for example, vaccines, bacterial adjuvants, and/or cytokines).

In passive immunotherapy, treatment involves the delivery of biologic reagents with established immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate anti-*Chlamydia* effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T lymphocytes (for example, CD8+ cytotoxic T-lymphocyte, CD4+ T-helper), killer cells (such as Natural Killer cells, lymphokine-activated killer cells), B cells, or antigen presenting cells (such as dendritic cells and macrophages) expressing the disclosed antigens. The polypeptides disclosed herein may also be used to generate antibodies or anti-idiotypic antibodies (as in U.S. Patent No. 4,918,164), for passive immunotherapy.

The predominant method of procuring adequate numbers of T-cells for adoptive immunotherapy is to grow immune T-cells *in vitro*. Culture conditions for expanding single antigen-specific T-cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. These *in vitro* culture conditions typically utilize intermittent stimulation with antigen, often in the presence of cytokines, such as IL-2, and non-dividing feeder cells. As noted above, the immunoreactive polypeptides described herein may be used to rapidly expand antigen-specific T cell cultures in order to generate sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast, or B-cells, may be pulsed with

immunoreactive polypeptides, or polynucleotide sequence(s) may be introduced into antigen presenting cells, using a variety of standard techniques well known in the art. For example, antigen presenting cells may be transfected or transduced with a polynucleotide sequence, wherein said sequence contains a promoter region appropriate for increasing expression, and can be expressed as part of a recombinant virus or other expression system. Several viral vectors may be used to transduce an antigen presenting cell, including pox virus, vaccinia virus, and adenovirus; also, antigen presenting cells may be transfected with polynucleotide sequences disclosed herein by a variety of means, including gene-gun technology, lipid-mediated delivery, electroporation, osmotic shock, and particulate delivery mechanisms, resulting in efficient and acceptable expression levels as determined by one of ordinary skill in the art. For cultured T-cells to be effective in therapy, the cultured T-cells must be able to grow and distribute widely and to survive long term *in vivo*. Studies have demonstrated that cultured T-cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (see, for example, Cheever, M., *et al.*, "Therapy With Cultured T Cells: Principles Revisited," *Immunological Reviews*, 157:177, 1997).

The polypeptides disclosed herein may also be employed to generate and/or isolate chlamydial-reactive T-cells, which can then be administered to the patient. In one technique, antigen-specific T-cell lines may be generated by *in vivo* immunization with short peptides corresponding to immunogenic portions of the disclosed polypeptides. The resulting antigen specific CD8+ or CD4+ T-cell clones may be isolated from the patient, expanded using standard tissue culture techniques, and returned to the patient.

Alternatively, peptides corresponding to immunogenic portions of the polypeptides may be employed to generate *Chlamydia* reactive T cell subsets by selective *in vitro* stimulation and expansion of autologous T cells to provide antigen-specific T cells which may be subsequently transferred to the patient as described, for example, by Chang *et al.* (*Crit. Rev. Oncol. Hematol.*, 22(3), 213, 1996). Cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as Isolex™ System, available from Nexell Therapeutics, Inc. Irvine, CA. The separated cells are stimulated with one or more of the immunoreactive

polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

In other embodiments, T-cell and/or antibody receptors specific for the polypeptides disclosed herein can be cloned, expanded, and transferred into other vectors or effector cells for use in adoptive immunotherapy. In particular, T cells may be transfected with the appropriate genes to express the variable domains from chlamydia specific monoclonal antibodies as the extracellular recognition elements and joined to the T cell receptor signaling chains, resulting in T cell activation, specific lysis, and cytokine release. This enables the T cell to redirect its specificity in an MHC-independent manner. See for example, Eshhar, Z., *Cancer Immunol Immunother*, 45(3-4):131-6, 1997 and Hwu, P., et al, *Cancer Res*, 55(15):3369-73, 1995. Another embodiment may include the transfection of chlamydia antigen specific alpha and beta T cell receptor chains into alternate T cells, as in Cole, DJ, et al, *Cancer Res*, 55(4):748-52, 1995.

In a further embodiment, syngeneic or autologous dendritic cells may be pulsed with peptides corresponding to at least an immunogenic portion of a polypeptide disclosed herein. The resulting antigen-specific dendritic cells may either be transferred into a patient, or employed to stimulate T cells to provide antigen-specific T cells which may, in turn, be administered to a patient. The use of peptide-pulsed dendritic cells to generate antigen-specific T cells and the subsequent use of such antigen-specific T cells to eradicate disease in a murine model has been demonstrated by Cheever et al, *Immunological Reviews*, 157:177, 1997). Additionally, vectors expressing the disclosed polynucleotides may be introduced into stem cells taken from the patient and clonally propagated *in vitro* for autologous transplant back into the same patient.

Within certain aspects, polypeptides, polynucleotides, T cells and/or binding agents disclosed herein may be incorporated into pharmaceutical compositions or immunogenic compositions (*i.e.*, vaccines). Pharmaceutical compositions comprise one or more such compounds and a physiologically acceptable carrier. Vaccines may comprise one or more such compounds and an immunostimulant. An immunostimulant may be any substance that enhances or potentiates an immune response to an exogenous antigen.

Examples of immunostimulants include adjuvants, biodegradable microspheres (e.g., polylactic galactide) and liposomes (into which the compound is incorporated; see e.g., Fullerton, U.S. Patent No. 4,235,877). Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Pharmaceutical compositions and vaccines within the scope of the present invention may also contain other compounds, which may be biologically active or inactive. For example, one or more immunogenic portions of other *Chlamydial* antigens may be present, either incorporated into a fusion polypeptide or as a separate compound, within the composition or vaccine.

A pharmaceutical composition or vaccine may contain DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As noted above, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, intravenous, intracranial, intraperitoneal, subcutaneous or intramuscular administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactate polyglycolate) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Such compositions may also comprise buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextran), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide) and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate. Compounds may also be encapsulated within liposomes using well known technology.

Any of a variety of immunostimulants may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Suitable adjuvants are commercially available

as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quill A. Cytokines, such as GM-CSF or interleukin-2, -7, or -12, may also be used as adjuvants.

Within the vaccines provided herein, under select circumstances, the adjuvant composition may be designed to induce an immune response predominantly of the Th1 type or Th2 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Preferred adjuvants for use in eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A (3D-MPL), together with an aluminum salt. MPL adjuvants are available from Ribi ImmunoChem Research Inc. (Hamilton, MT) (see US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555. Another preferred adjuvant is a saponin, preferably QS21, which may be used alone or in combination with other adjuvants. For example, an enhanced system involves the combination of a monophosphoryl lipid A and saponin derivative, such as the combination of QS21 and 3D-MPL as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in WO 96/33739. Other preferred formulations

comprises an oil-in-water emulsion and tocopherol. A particularly potent adjuvant formulation involving QS21, 3D-MPL and tocopherol in an oil-in-water emulsion is described in WO 95/17210. Any vaccine provided herein may be prepared using well known methods that result in a combination of antigen, immune response enhancer and a suitable carrier or excipient.

The compositions described herein may be administered as part of a sustained release formulation (*i.e.*, a formulation such as a capsule, sponge or gel (composed of polysaccharides, for example) that effects a slow release of compound following administration). Such formulations may generally be prepared using well known technology and administered by, for example, oral, rectal or subcutaneous implantation, or by implantation at the desired target site. Sustained-release formulations may contain a polypeptide, polynucleotide or antibody dispersed in a carrier matrix and/or contained within a reservoir surrounded by a rate controlling membrane. Carriers for use within such formulations are biocompatible, and may also be biodegradable; preferably the formulation provides a relatively constant level of active component release. The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

Any of a variety of delivery vehicles may be employed within pharmaceutical compositions and vaccines to facilitate production of an antigen-specific immune response that targets *Chlamydia*-infected cells. Delivery vehicles include antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-*Chlamydia* effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs

(Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to be effective as a physiological adjuvant for eliciting prophylactic or therapeutic immunity (see Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency, and their ability to activate naïve T cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (see Zitvogel et al., *Nature Med.* 4:594-600, 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation, maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide encoding a

*Chlamydial* protein (or portion or other variant thereof) such that the *Chlamydial* polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a composition or vaccine comprising such transfected cells may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the *Chlamydial* polypeptide, DNA (naked or within a plasmid vector) or RNA; or with antigen-expressing recombinant bacterium or viruses (e.g., vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (e.g., a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

Routes and frequency of administration of pharmaceutical compositions and vaccines, as well as dosage, will vary from individual to individual. In general, the pharmaceutical compositions and vaccines may be administered by injection (e.g., intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (e.g., by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable of raising an immune response in an immunized patient sufficient to protect the patient from *Chlamydial* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 µg. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a *Chlamydial* protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples obtained from a patient before and after treatment.

In another aspect, the present invention provides methods for using the polypeptides described above to diagnose Chlamydial infection. In this aspect, methods are provided for detecting Chlamydial infection in a biological sample, using one or more of the above polypeptides, either alone or in combination. For clarity, the term "polypeptide" will be used when describing specific embodiments of the inventive diagnostic methods. However, it will be clear to one of skill in the art that the fusion proteins of the present invention may also be employed in such methods.

As used herein, a "biological sample" is any antibody-containing sample obtained from a patient. Preferably, the sample is whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid or urine. More preferably, the sample is a blood, serum or plasma sample obtained from a patient. The polypeptides are used in an assay, as described below, to determine the presence or absence of antibodies to the polypeptide(s) in the sample, relative

to a predetermined cut-off value. The presence of such antibodies indicates previous sensitization to *Chlamydia* antigens which may be indicative of *Chlamydia*-infection.

In embodiments in which more than one polypeptide is employed, the polypeptides used are preferably complementary (*i.e.*, one component polypeptide will tend to detect infection in samples where the infection would not be detected by another component polypeptide). Complementary polypeptides may generally be identified by using each polypeptide individually to evaluate serum samples obtained from a series of patients known to be infected with *Chlamydia*. After determining which samples test positive (as described below) with each polypeptide, combinations of two or more polypeptides may be formulated that are capable of detecting infection in most, or all, of the samples tested.

A variety of assay formats are known to those of ordinary skill in the art for using one or more polypeptides to detect antibodies in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988, which is incorporated herein by reference. In a preferred embodiment, the assay involves the use of polypeptide immobilized on a solid support to bind to and remove the antibody from the sample. The bound antibody may then be detected using a detection reagent that contains a reporter group. Suitable detection reagents include antibodies that bind to the antibody/polypeptide complex and free polypeptide labeled with a reporter group (*e.g.*, in a semi-competitive assay). Alternatively, a competitive assay may be utilized, in which an antibody that binds to the polypeptide is labeled with a reporter group and allowed to bind to the immobilized antigen after incubation of the antigen with the sample. The extent to which components of the sample inhibit the binding of the labeled antibody to the polypeptide is indicative of the reactivity of the sample with the immobilized polypeptide.

The solid support may be any solid material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate, or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681.

The polypeptides may be bound to the solid support using a variety of techniques known to those of ordinary skill in the art. In the context of the present invention, the term "bound" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Binding by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the polypeptide, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of polypeptide ranging from about 10 ng to about 1  $\mu$ g, and preferably about 100 ng, is sufficient to bind an adequate amount of antigen.

Covalent attachment of polypeptide to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the polypeptide. For example, the polypeptide may be bound to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the polypeptide (*see, e.g.*, Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is an enzyme linked immunosorbent assay (ELISA). This assay may be performed by first contacting a polypeptide antigen that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that antibodies to the polypeptide within the sample are allowed to bind to the immobilized polypeptide. Unbound sample is then removed from the immobilized polypeptide and a detection reagent capable of binding to the immobilized antibody-polypeptide complex is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific detection reagent.

More specifically, once the polypeptide is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin (BSA) or Tween 20<sup>TM</sup> (Sigma Chemical Co., St. Louis, MO) may be employed. The

immobilized polypeptide is then incubated with the sample, and antibody is allowed to bind to the antigen. The sample may be diluted with a suitable dilutent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of antibody within an HGE-infected sample. Preferably, the contact time is sufficient to achieve a level of binding that is at least 95% of that achieved at equilibrium between bound and unbound antibody. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20<sup>TM</sup>. Detection reagent may then be added to the solid support. An appropriate detection reagent is any compound that binds to the immobilized antibody-polypeptide complex and that can be detected by any of a variety of means known to those in the art. Preferably, the detection reagent contains a binding agent (such as, for example, Protein A, Protein G, immunoglobulin, lectin or free antigen) conjugated to a reporter group. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of binding agent to reporter group may be achieved using standard methods known to those of ordinary skill in the art. Common binding agents may also be purchased conjugated to a variety of reporter groups from many commercial sources (*e.g.*, Zymed Laboratories, San Francisco, CA, and Pierce, Rockford, IL).

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound antibody. An appropriate amount of time may generally be determined from the manufacturer's instructions or by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods

are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of anti-*Chlamydia* antibodies in the sample, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antigen is incubated with samples from an uninfected patient. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for *Chlamydia*-infection. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, pp. 106-107. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for Chlamydial infection.

In a related embodiment, the assay is performed in a rapid flow-through or strip test format, wherein the antigen is immobilized on a membrane, such as nitrocellulose. In the flow-through test, antibodies within the sample bind to the immobilized polypeptide as the sample passes through the membrane. A detection reagent (*e.g.*, protein A-colloidal gold) then binds to the antibody-polypeptide complex as the solution containing the detection reagent flows through the membrane. The detection of bound detection reagent may then be

performed as described above. In the strip test format, one end of the membrane to which polypeptide is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing detection reagent and to the area of immobilized polypeptide. Concentration of detection reagent at the polypeptide indicates the presence of anti-*Chlamydia* antibodies in the sample. Typically, the concentration of detection reagent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of polypeptide immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of antibodies that would be sufficient to generate a positive signal in an ELISA, as discussed above. Preferably, the amount of polypeptide immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount (*e.g.*, one drop) of patient serum or blood.

Of course, numerous other assay protocols exist that are suitable for use with the polypeptides of the present invention. The above descriptions are intended to be exemplary only. One example of an alternative assay protocol which may be usefully employed in such methods is a Western blot, wherein the proteins present in a biological sample are separated on a gel, prior to exposure to a binding agent. Such techniques are well known to those of skill in the art.

The present invention further provides agents, such as antibodies and antigen-binding fragments thereof, that specifically bind to a *Chlamydial* protein. As used herein, an antibody, or antigen-binding fragment thereof, is said to "specifically bind" to a *Chlamydial* protein if it reacts at a detectable level (within, for example, an ELISA) with a *Chlamydial* protein, and does not react detectably with unrelated proteins under similar conditions. As used herein, "binding" refers to a noncovalent association between two separate molecules such that a complex is formed. The ability to bind may be evaluated by, for example, determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind," in the context of the present invention, when the binding constant for complex formation exceeds about  $10^3$

L/mol. The binding constant may be determined using methods well known in the art.

Binding agents may be further capable of differentiating between patients with and without a *Chlamydial* infection using the representative assays provided herein. In other words, antibodies or other binding agents that bind to a *Chlamydial* protein will generate a signal indicating the presence of a *Chlamydial* infection in at least about 20% of patients with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without infection. To determine whether a binding agent satisfies this requirement, biological samples (e.g., blood, sera, sputum urine and/or tissue biopsies) from patients with and without *Chlamydial* infection (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. It will be apparent that a statistically significant number of samples with and without the disease should be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep or goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and

the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Within certain embodiments, the use of antigen-binding fragments of antibodies may be preferred. Such fragments include Fab fragments, which may be prepared using standard techniques. Briefly, immunoglobulins may be purified from rabbit serum by affinity chromatography on Protein A bead columns (Harlow and Lane, *Antibodies: A*

*Laboratory Manual*, Cold Spring Harbor Laboratory, 1988) and digested by papain to yield Fab and Fc fragments. The Fab and Fc fragments may be separated by affinity chromatography on protein A bead columns.

Monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include <sup>90</sup>Y, <sup>123</sup>I, <sup>125</sup>I, <sup>131</sup>I, <sup>186</sup>Re, <sup>188</sup>Re, <sup>211</sup>At, and <sup>212</sup>Bi. Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulphhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion

of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or

in site-specific regions by appropriate methods. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density, and the rate of clearance of the antibody.

Antibodies may be used in diagnostic tests to detect the presence of *Chlamydia* antigens using assays similar to those detailed above and other techniques well known to those of skill in the art, thereby providing a method for detecting Chlamydial infection in a patient.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify *Chlamydia*-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a polypeptide of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a polypeptide of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule encoding one of the polypeptides disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may thus be used to detect *Chlamydia*-specific sequences in biological samples. DNA probes or primers

comprising oligonucleotide sequences described above may be used alone or in combination with each other.

The following Examples are offered by way of illustration and not by way of limitation.

#### EXAMPLE 1

##### ISOLATION OF DNA SEQUENCES ENCODING CHLAMYDIA ANTIGENS

*Chlamydia* antigens of the present invention were isolated by expression cloning of a genomic DNA library of *Chlamydia trachomatis* LGV II essentially as described by Sanderson et al. (*J. Exp. Med.*, 1995, 182:1751-1757) and were shown to induce PBMC proliferation and IFN- $\gamma$  in an immunoreactive T cell line.

A *Chlamydia*-specific T cell line was generated by stimulating PBMCs from a normal donor with no history of chlamydial genital tract infection with elementary bodies of *Chlamydia trachomatis* LGV II. This T cell line, referred to as TCL-8, was found to recognize both *Chlamydia trachomatis* and *Chlamydia pneumoniae* infected monocyte-derived dendritic cells.

A randomly sheared genomic library of *Chlamydia trachomatis* LGV II was constructed in Lambda ZAP (Stratagene, La Jolla, CA) and the amplified library plated out in 96 well microtiter plates at a density of 30 clones/well. Bacteria were induced to express recombinant protein in the presence of 2 mM IPTG for 3 h, then pelleted and resuspended in 200  $\mu$ l of RPMI 10% FBS. 10  $\mu$ l of the induced bacterial suspension was transferred to 96 well plates containing autologous monocyte-derived dendritic cells. After a 2 h incubation, dendritic cells were washed to remove free *E. coli* and *Chlamydia*-specific T cells were added. Positive *E. coli* pools were identified by determining IFN- $\gamma$  production and proliferation of the T cells in response to the pools.

Four positive pools were identified, which were broken down to yield four pure clones (referred to as 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31), with insert sizes of 481 bp, 183 bp, 110 bp and 1400 bp, respectively. The determined DNA sequences for 1-B1-66, 4-D7-28, 3-G3-10 and 10-C10-31 are provided in SEQ ID NO: 1-4, respectively. Clone 1-B1-66 is approximately in region 536690 of the *C. trachomatis* genome (NCBI C.

*trachomatis* database). Within clone 1-B1-66, an open reading frame (ORF) has been identified (nucleotides 115 - 375) that encodes a previously identified 9 kDa protein (Stephens, et al. Genbank Accession No. AE001320), the sequence of which is provided in SEQ ID NO: 5). Clone 4-D7-28 is a smaller region of the same ORF (amino acids 22-82 of 1-B1-66). Clone 3-G3-10 is approximately in region 74559 of the *C. trachomatis* genome. The insert is cloned in the antisense orientation with respect to its orientation in the genome. The clone 10-C10-31 contains an open reading frame that corresponds to a previously published sequence for S13 ribosomal protein from *Chlamydia trachomatis* (Gu, L. et al. *J. Bacteriology*, 177:2594-2601, 1995). The predicted protein sequences for 4-D7-28 and 10-C10-31 are provided in SEQ ID NO: 6 and 12, respectively. Predicted protein sequences for 3-G3-10 are provided in SEQ ID NO: 7-11.

In a related series of screening studies, an additional T cell line was used to screen the genomic DNA library of *Chlamydia trachomatis* LGV II described above. A *Chlamydia*-specific T cell line (TCT-1) was derived from a patient with a chlamydial genital tract infection by stimulating patient PBMC with autologous monocyte-derived dendritic cells infected with elementary bodies of *Chlamydia trachomatis* LGV II. One clone, 4C9-18 (SEQ ID NO: 21), containing a 1256 bp insert, elicited a specific immune response, as measured by standard proliferation assays, from the *Chlamydia*-specific T cell line TCT-1. Subsequent analysis revealed this clone to contain three known sequences: lipoamide dehydrogenase (Genbank Accession No. AE001326), disclosed in SEQ ID NO: 22; a hypothetical protein CT429 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 23; and part of an open reading frame of ubiquinone methyltransferase CT428 (Genbank Accession No. AE001316), disclosed in SEQ ID NO: 24.

In further studies involving clone 4C9-18 (SEQ ID NO: 21), the full-length amino acid sequence for lipoamide dehydrognase (SEQ ID NO: 22) from *C. trachomatis* (LGV II) was expressed in clone CtL2-LPDA-FL, as disclosed in SEQ ID NO: 90.

To further characterize the open reading frame containing the T cell stimulating epitope(s), a cDNA fragment containing nucleotides 1-695 of clone 4C9-18 with a cDNA sequence encoding a 6X-Histidine tag on the amino terminus was subcloned into the NdeI/EcoRI site of the pET17b vector (Novagen, Madison, WI), referred to as clone 4C9-

18#2 BL21 pLysS (SEQ ID NO: 25, with the corresponding amino acid sequence provided in SEQ ID NO: 26) and transformed into *E. coli*. Selective induction of the transformed *E. coli* with 2 mM IPTG for three hours resulted in the expression of a 26 kDa protein from clone 4C9-18#2 BL21 pLysS, as evidenced by standard Coomassie-stained SDS-PAGE. To determine the immunogenicity of the protein encoded by clone 4C9-18#2 BL21 pLysS, *E. coli* expressing the 26 kDa protein were titered onto  $1 \times 10^4$  monocyte-derived dendritic cells and incubated for two hours. The dendritic cell cultures were washed and  $2.5 \times 10^4$  T cells (TCT-1) added and allowed to incubate for an additional 72 hours, at which time the level of IFN- $\gamma$  in the culture supernatant was determined by ELISA. As shown in Fig. 1, the T-cell line TCT-1 was found to respond to induced cultures as measured by IFN-g, indicating a *Chlamydia*-specific T-cell response against the lipoamide dehydrogenase sequence. Similarly, the protein encoded by clone 4C9-18#2 BL21 pLysS was shown to stimulate the TCT-1 T-cell line by standard proliferation assays.

Subsequent studies to identify additional *Chlamydia trachomatis* antigens using the above-described CD4+ T-cell expression cloning technique yielded additional clones. The TCT-1 and TCL-8 *Chlamydia*-specific T-cell lines, as well as the TCP-21 T-cell line were utilized to screen the *Chlamydia trachomatis* LGVII genomic library. The TCP-21 T-cell line was derived from a patient having a humoral immune response to *Chlamydia pneumoniae*. The TCT-1 cell line identified 37 positive pools, the TCT-3 cell line identified 41 positive pools and the TCP-21 cell line identified 2 positive pools. The following clones were derived from 10 of these positive pools. Clone 11-A3-93 (SEQ ID NO: 64), identified by the TCP-21 cell line, is a 1339 bp genomic fragment sharing homology to the HAD superfamily (CT103). The second insert in the same clone shares homology with the fab I gene (CT104) present on the complementary strand. Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*.

Clone 11-G10-46, (SEQ ID NO: 62), identified using the TCT-3 cell line, contains a 688 bp insert that shares homology to the hypothetical protein CT610. Clone 11-G1-34, (SEQ ID NO: 61), identified using the TCT-3 cell line, has two partial open reading

frames (ORF) with an insert size of 1215 bp. One ORF shares homology to the malate dehydrogenase gene (CT376), and the other ORF shares homology to the glycogen hydrolase gene (CT042). Clone 11-H3-68, (SEQ ID NO: 60), identified using the TCT-3 cell line, has two ORFs with a total insert size of 1180 bp. One partial ORF encodes the plasmid-encoded PGP6-D virulence protein while the second ORF is a complete ORF for the L1 ribosomal gene (CT318). Clone 11-H4-28, (SEQ ID NO: 59), identified using the TCT-3 cell line, has an insert size of 552 bp and is part of the ORF for the dnaK gene (CT396). Clone 12-B3-95, (SEQ ID NO: 58), identified using the TCT-1 cell line, has an insert size of 463 bp and is a part of the ORF for the lipoamide dehydrogenase gene (CT557). Clones 15-G1-89 and 12-B3-95 are identical, (SEQ ID NO: 55 and 58, respectively), identified using the TCT-1 cell line, has an insert size of 463 bp and is part of the ORF for the lipoamide dehydrogenase gene (CT557). Clone 12-G3-83, (SEQ ID NO: 57), identified using the TCT-1 cell line, has an insert size of 1537 bp and has part of the ORF for the hypothetical protein CT622.

Clone 23-G7-68, (SEQ ID NO: 79), identified using the TCT-3 cell line, contains a 950 bp insert and contains a small part of the L11 ribosomal ORF, the entire ORF for L1 ribosomal protein and a part of the ORF for L10 ribosomal protein. Clone 22-F8-91, (SEQ ID NO: 80), identified using the TCT-1 cell line, contains a 395 bp insert that contains a part of the pmpC ORF on the complementary strand of the clone. Clone 21-E8-95, (SEQ ID NO: 81), identified using the TCT-3 cell line, contains a 2,085 bp insert which contains part of CT613 ORF, the complete ORF for CT612, the complete ORF for CT611 and part of the ORF for CT610. Clone 19-F12-57, (SEQ ID NO: 82), identified using the TCT-3 cell line, contains a 405 bp insert which contains part of the CT 858 ORF and a small part of the recA ORF. Clone 19-F12-53, (SEQ ID NO: 83), identified using the TCT-3 cell line, contains a 379 bp insert that is part of the ORF for CT455 encoding glutamyl tRNA synthetase. Clone 19-A5-54, (SEQ ID NO: 84), identified using the TCT-3 cell line, contains a 715 bp insert that is part of the ORF3 (complementary strand of the clone) of the cryptic plasmid. Clone 17-E11-72, (SEQ ID NO: 85), identified using the TCT-1 cell line, contains a 476 bp insert that is part of the ORF for Opp\_2 and pmpD. The pmpD region of this clone is covered by the pmpD region of clone 15-H2-76. Clone 17-C1-77, (SEQ ID NO: 86), identified using the TCT-3 cell line, contains a 1551 bp insert that is part of the CT857 ORF, as well as part of

the CT858 ORF. Clone 15-H2-76, (SEQ ID NO: 87), identified using the TCT-1 cell line, contains a 3,031 bp insert that contains a large part of the pmpD ORF, part of the CT089 ORF, as well as part of the ORF for SycE. Clone 15-A3-26, (SEQ ID NO: 88), contains a 976 bp insert that contains part of the ORF for CT858. Clone 17-G4-36, (SEQ ID NO: 267), identified using the TCT-10 cell line, contains a 680 bp insert that is in frame with beta-gal in the plasmid and shares homology to part of the ORF for DNA-directed RNA polymerase beta subunit (CT315 in SerD).

Several of the clones described above share homology to various polymorphic membrane proteins. The genomic sequence of *Chlamydia trachomatis* contains a family of nine polymorphic membrane protein genes, referred to as pmp. These genes are designated pmpA, pmpB, pmpC, pmpD, pmpE, pmpF, pmpG, pmpH and pmpI. Proteins expressed from these genes are believed to be of biological relevance in generating a protective immune response to a *Chlamydial* infection. In particular, pmpC, pmpD, pmpE and pmpI contain predictable signal peptides, suggesting they are outer membrane proteins, and therefore, potential immunological targets.

Based on the *Chlamydia trachomatis* LGVII serovar sequence, primer pairs were designed to PCR amplify the full-length fragments of pmpC, pmpD, pmpE, pmpG, pmpH and pmpI. The resulting fragments were subcloned into the DNA vaccine vector JA4304 or JAL, which is JA4304 with a modified linker (SmithKline Beecham, London, England). Specifically, PmpC was subcloned into the JAL vector using the 5' oligo GAT AGG CGC GCC GCA ATC ATG AAA TTT ATG TCA GCT ACT GCT G and the 3' oligo CAG AAC GCG TTT AGA ATG TCA TAC GAG CAC CGC A, as provided in SEQ ID NO: 197 and 198, respectively. PCR amplification of the gene under conditions well known in the art and ligation into the 5' ASCI/3' MluI sites of the JAL vector was completed after inserting the short nucleotide sequence GCAATC (SEQ ID NO: 199) upstream of the ATG to create a Kozak-like sequence. The resulting expression vector contained the full-length pmpC gene comprising 5325 nucleotides (SEQ ID NO: 173) containing the hypothetical signal sequence, which encodes a 187 kD protein (SEQ ID NO: 179). The pmpD gene was subcloned into the JA4304 vaccine vector following PCR amplification of the gene using the following oligos: 5' oligo- TGC AAT CAT GAG TTC GCA GAA AGA TAT AAA AAG C

(SEQ ID NO: 200) and 3' oligo- CAG AGC TAG CTT AAA AGA TCA ATC GCA ATC CAG TAT TC (SEQ ID NO: 201). The gene was ligated into the a 5' blunted HIII/3' MluI site of the JA4304 vaccine vector using standard techniques well known in the art. The CAATC (SEQ ID NO: 202) was inserted upstream of the ATG to create a Kozak-like sequence. This clone is unique in that the last threonine of the HindIII site is missing due to the blunting procedure, as is the last glycine of the Kozak-like sequence. The insert, a 4593 nucleotide fragment (SEQ ID NO: 172) is the full-length gene for pmpD containing the hypothetical signal sequence, which encodes a 161 kD protein (SEQ ID NO: 178). PmpE was subcloned into the JA4304 vector using the 5' oligo- TGC AAT CAT GAA AAA AGC GTT TTT CTT TTT C (SEQ ID NO: 203), and the 3' oligo- CAG AAC GCG TCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 204). Following PCR amplification, the gene was ligated into the 5' blunted HIII/3' MluI site of JA4304. To facilitate this, a short nucleotide sequence, TGCAATC (SEQ ID NO: 293), was added upstream of the initiation codon for creating a Kozak-like sequence and reconstituting the HindIII site. The insert is the full-length pmpE gene (SEQ ID NO: 171) containing the hypothetical signal sequence. The pmpE gene encodes a 105 kD protein (SEQ ID NO: 177). The pmpG gene was PCR amplified using the 5' oligo- GTG CAA TCA TGA TTC CTC AAG GAA TTT ACG ( SEQ ID NO: 205), and the 3' oligo- CAG AAC GCG TTT AGA ACC GGA CTT TAC TTC C (SEQ ID NO: 206) and subcloned into the JA4304 vector. Similar cloning strategies were followed for the pmpI and pmpK genes. In addition, primer pairs were designed to PCR amplify the full-length or overlapping fragments of the pmp genes, which were then subcloned for protein expression in the pET17b vector (Novagen, Madison, WI) and transfected into E. coli BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Several of the genes encoding the recombinant proteins, as described below, lack the native signal sequence to facilitate expression of the protein. Full-length protein expression of pmpC was accomplished through expression of two overlapping fragments, representing the amino and carboxy termini. Subcloning of the pmpC-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 187, with the corresponding amino acid sequence provided in SEQ ID NO: 195) used the 5' oligo- CAG ACA TAT GCA TCA CCA TCA CCA TCA CGA

GGC GAG CTC GAT CCA AGA TC (SEQ ID NO: 207), and the 3' oligo- CAG AGG TAC CTC AGA TAG CAC TCT CTC CTA TTA AAG TAG G (SEQ ID NO: 208) into the 5' NdeI/3' KPN cloning site of the vector. The carboxy terminus portion of the gene, pmpC-carboxy terminal fragment (SEQ ID NO: 186, with the corresponding amino acid sequence provided in SEQ ID NO: 194), was subcloned into the 5' NheI/3' KPN cloning site of the expression vector using the following primers: 5' oligo- CAG AGC TAG CAT GCA TCA CCA TCA CCA TCA CGT TAA GAT TGA GAA CTT CTC TGG C (SEQ ID NO: 209), and 3' oligo- CAG AGG TAC CTT AGA ATG TCA TAC GAG CAC CGC AG (SEQ ID NO: 210). PmpD was also expressed as two overlapping proteins. The pmpD-amino terminal portion, which lacks the signal sequence, (SEQ ID NO: 185, with the corresponding amino acid sequence provided in SEQ ID NO: 193) contains the initiating codon of the pET17b and is expressed as a 80 kD protein. For protein expression and purification purposes, a six-histidine tag follows the initiation codon and is fused at the 28<sup>th</sup> amino acid (nucleotide 84) of the gene. The following primers were used, 5' oligo, CAG ACA TAT GCA TCA CCA TCA CCA TCA CGG GTT AGC (SEQ ID NO: 211), and the 3' oligo- CAG AGG TAC CTC AGC TCC TCC AGC ACA CTC TCT TC (SEQ ID NO: 212), to splice into the 5' NdeI/3' KPN cloning site of the vector. The pmpD-carboxy terminus portion (SEQ ID NO: 184) was expressed as a 92 kD protein (SEQ ID NO: 192). For expression and subsequent purification, an additional methionine, alanine and serine was included, which represent the initiation codon and the first two amino acids from the pET17b vector. A six-histidine tag downstream of the methionine, alanine and serine is fused at the 691<sup>st</sup> amino acid (nucleotide 2073) of the gene. The 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CGG TGC TAT TTC TTG CTT ACG TGG (SEQ ID NO: 213) and the 3' oligo- CAG AGG TAC TTn AAA AGA TCA ATC GCA ATC CAG TAT TCG (SEQ ID NO: 214) were used to subclone the insert into the 5' NheI/3' KPN cloning site of the expression vector. PmpE was expressed as a 106kD protein (SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191). The pmpE insert also lacks the native signal sequence. PCR amplification of the gene under conditions well known in the art was performed using the following oligo primers: 5' oligo- CAG AGG ATC CAC ATC ACC ATC ACC ATC ACG GAC TAG CTA GAG AGG TTC (SEQ ID NO: 215), and

the 3' oligo- CAG AGA ATT CCT AGA ATC GCA GAG CAA TTT C (SEQ ID NO: 216), and the amplified insert was ligated into a 5' BamHI/3' EcoRI site of JA4304. The short nucleotide sequence, as provided in SEQ ID NO: 217, was inserted upstream of the initiation codon for creating the Kozak-like sequence and reconstituting the HindIII site. The expressed protein contains the initiation codon and the downstream 21 amino acids from the pET17b expression vector, i.e., MASMTGGQQMGRDSSLVPSSDP (SEQ ID NO: 218). In addition, a six-histidine tag is included upstream of the sequence described above and is fused at the 28<sup>th</sup> amino acid (nucleotide 84) of the gene, which eliminates the hypothetical signal peptide. The sequences provided in SEQ ID NO: 183 with the corresponding amino acid sequence provided in SEQ ID NO: 191 do not include these additional sequences. The pmpG gene (SEQ ID NO: 182, with the corresponding amino acid sequence provided in SEQ ID No; 190) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGG TAC CGC ATC ACC ATC ACC ATC ACA TGA TTC CTC AAG GAA TTT ACG (SEQ ID NO: 219), and the 3' oligo- CAG AGC GGC CGC TTA GAA CCG GAC TTT ACT TCC (SEQ ID NO: 220), and ligated into the 5' KPN/3' NotI cloning site of the expression vector. The expressed protein contains an additional amino acid sequence at the amino end, namely, MASMTGGQQNGRDSSLVPHHHHHH (SEQ ID NO: 221), which comprises the initiation codon and additional sequence from the pET17b expression vector. The pmpI gene (SEQ ID NO: 181, with the corresponding amino acid sequence provided in SEQ ID No; 189) was PCR amplified under conditions well known in the art using the following oligo primers: 5' oligo- CAG AGC TAG CCA TCA CCA TCA CCA TCA CCT CTT TGG CCA GGA TCC C (SEQ ID NO: 222), and the 3' oligo- CAG AAC TAG TCT AGA ACC TGT AAG TGG TCC (SEQ ID NO: 223), and ligated into the expression vector at the 5' NheI/3' SpeI cloning site. The 95 kD expressed protein contains the initiation codon plus an additional alanine and serine from the pET17b vector at the amino end of the protein. In addition, a six-histidine tag is fused at the 21<sup>st</sup> amino acid of the gene, which eliminates the hypothetical signal peptide.

Clone 14H1-4, (SEQ ID NO: 56), identified using the TCT-3 cell line, contains a complete ORF for the TSA gene, thiol specific antioxidant – CT603 (the CT603 ORF is a homolog of CPn0778 from *C. pneumoniae*). The TSA open reading frame in clone

14-H1-4 was amplified such that the expressed protein possess an additional methionine and a 6x histidine tag (amino terminal end). This amplified insert was sub-cloned into the Nde/EcoRI sites of the pET17b vector. Upon induction of this clone with IPTG, a 22.6 kDa protein was purified by Ni-NTA agarose affinity chromatography. The determined amino acid sequence for the 195 amino acid ORF of clone 14-H1-4 encoding the TSA gene is provided in SEQ ID NO: 65. Further analysis yielded a full-length clone for the TSA gene, referred to as CTL2-TSA-FL, with the full-length amino acid sequence provided in SEQ ID NO: 92.

Further studies yielded 10 additional clones identified by the TCT-1 and TCT-3 T-cell lines, as described above. The clones identified by the TCT-1 line are: 16-D4-22, 17-C5-19, 18-C5-2, 20-G3-45 and 21-C7-66; clones identified by the TCT-3 cell line are: 17-C10-31, 17-E2-9, 22-A1-49 and 22-B3-53. Clone 21-G12-60 was recognized by both the TCT-1 and TCT-3 T cell lines. Clone 16-D4-22 (SEQ ID NO: 119), identified using the TCT-1 cell line contains a 953 bp insert that contains two genes, parts of open reading frame 3 (ORF3) and ORF4 of the *C. trachomatis* plasmid for growth within mammalian cells. Clone 17-C5-19 (SEQ ID NO: 118), contains a 951 bp insert that contains part of the ORF for DT431, encoding for clpP\_1 protease and part of the ORF for CT430 (diaminopimelate epimerase). Clone 18-C5-2 (SEQ ID NO: 117) is part of the ORF for S1 ribosomal protein with a 446 bp insert that was identified using the TCT-1 cell line. Clone 20-G3-45 (SEQ ID NO: 116), identified by the TCT-1 cell line, contains a 437 bp insert that is part of the pmpB gene (CT413). Clone 21-C7-66 (SEQ ID NO: 115), identified by the TCT-1 line, contains a 995bp insert that encodes part of the dnaK like protein. The insert of this clone does not overlap with the insert of the TCT-3 clone 11-H4-28 (SEQ ID NO: 59), which was shown to be part of the dnaK gene CT396. Clone 17-C10-31 (SEQ ID NO: 114), identified by the TCT-3 cell line, contains a 976 bp insert. This clone contains part of the ORF for CT858, a protease containing IRBP and DHR domains. Clone 17-E2-9 (SEQ ID NO: 113) contains part of ORFs for two genes, CT611 and CT610, that span a 1142 bp insert. Clone 22-A1-49 (SEQ ID NO: 112), identified using the TCT-3 line, also contains two genes in a 698 bp insert. Part of the ORF for CT660 (DNA gyrase{gyrA\_2}) is present on the top strand whereas the complete ORF for a hypothetical protein CT659 is present on the complementary

strand. Clone 22-B3-53 (SEQ ID NO: 111), identified by the TCT-1 line, has a 267 bp insert that encodes part of the ORF for GroEL (CT110). Clone 21-G12-60 (SEQ ID NO: 110), identified by both the TCT-1 and TCT-3 cell lines contains a 1461 bp insert that contains partial ORFs for hypothetical proteins CT875, CT229 and CT228.

Additional *Chlamydia* antigens were obtained by screening a genomic expression library of *Chlamydia trachomatis* (LGV II serovar) in Lambda Screen-1 vector (Novagen, Madison, WI) with sera pooled from several *Chlamydia*-infected individuals using techniques well known in the art. The following immuno-reactive clones were identified and the inserts containing *Chlamydia* genes sequenced: CTL2#1 (SEQ ID NO: 71); CTL2#2 (SEQ ID NO: 70); CTL2#3-5' (SEQ ID NO: 72, a first determined genomic sequence representing the 5' end); CTL2#3-3' (SEQ ID NO: 73, a second determined genomic sequence representing the 3' end); CTL2#4 (SEQ ID NO: 53); CTL2#5 (SEQ ID NO: 69); CTL2#6 (SEQ ID NO: 68); CTL2#7 (SEQ ID NO: 67); CTL2#8b (SEQ ID NO: 54); CTL2#9 (SEQ ID NO: 66); CTL2#10-5' (SEQ ID NO: 74, a first determined genomic sequence representing the 5' end); CTL2#10-3' (SEQ ID NO: 75, a second determined genomic sequence representing the 3' end); CTL2#11-5' (SEQ ID NO: 45, a first determined genomic sequence representing the 5' end); CTL2#11-3' (SEQ ID NO: 44, a second determined genomic sequence representing the 3' end); CTL2#12 (SEQ ID NO: 46); CTL2#16-5' (SEQ ID NO: 47); CTL2#18-5' (SEQ ID NO: 49, a first determined genomic sequence representing the 5' end); CTL2#18-3' (SEQ ID NO: 48, a second determined genomic sequence representing the 3' end); CTL2#19-5' (SEQ ID NO: 76, the determined genomic sequence representing the 5' end); CTL2#21 (SEQ ID NO: 50); CTL2#23 (SEQ ID NO: 51; and CTL2#24 (SEQ ID NO: 52).

Additional *Chlamydia trachomatis* antigens were identified by serological expression cloning. These studies used sera pooled from several *Chlamydia*-infected individuals, as described above, but, IgA, and IgM antibodies were used in addition to IgG as a secondary antibody. Clones screened by this method enhance detection of antigens recognized by an early immune response to a *Chlamydial* infection, that is a mucosal humoral immune response. The following immunoreactive clones were characterized and the inserts containing *Chlamydia* genes sequenced: CTL2gam-1 (SEQ ID NO: 290), CTL2gam-2 (SEQ

ID NO: 289), CTL2gam-5 (SEQ ID NO: 288), CTL2gam-6-3' (SEQ ID NO: 287, a second determined genomic sequence representing the 3' end), CTL2gam-6-5' (SEQ ID NO: 286, a first determined genomic sequence representing the 5' end), CTL2gam-8 (SEQ ID NO: 285), CTL2gam-10 (SEQ ID NO: 284), CTL2gam-13 (SEQ ID NO: 283), CTL2gam-15-3' (SEQ ID NO: 282, a second determined genomic sequence representing the 3' end), CTL2gam-15-5' (SEQ ID NO: 281, a first determined genomic sequence representing the 5' end), CTL2gam-17 (SEQ ID NO: 280), CTL2gam-18 (SEQ ID NO: 279), CTL2gam-21 (SEQ ID NO: 278), CTL2gam-23 (SEQ ID NO: 277), CTL2gam-24 (SEQ ID NO: 276), CTL2gam-26 (SEQ ID NO: 275), CTL2gam-27 (SEQ ID NO: 274), CTL2gam-28 (SEQ ID NO: 273), CTL2gam-30-3' (SEQ ID NO: 272, a second determined genomic sequence representing the 3' end) and CTL2gam-30-5' (SEQ ID NO: 271, a first determined genomic sequence representing the 5' end).

## EXAMPLE 2

### INDUCTION OF T CELL PROLIFERATION AND INTERFERON- $\gamma$ PRODUCTION BY CHLAMYDIA TRACHOMATIS ANTIGENS

The ability of recombinant *Chlamydia trachomatis* antigens to induce T cell proliferation and interferon- $\gamma$  production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatograph (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. trachomatis* patients as well as from normal donors whose T-cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50  $\mu$ g/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10  $\mu$ g/mL. After six days of culture in 96-well round-bottom plates in a volume of 200  $\mu$ l, 50  $\mu$ l of medium is removed from each well for determination of IFN- $\gamma$  levels, as described below. The plates are then pulsed with 1  $\mu$ Ci/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that

result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN- $\gamma$  is measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN- $\gamma$  (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN- $\gamma$  serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

Using the above methodology, recombinant 1B1-66 protein (SEQ ID NO: 5) as well as two synthetic peptides corresponding to amino acid residues 48-67 (SEQ ID NO: 13; referred to as 1-B1-66/48-67) and 58-77 (SEQ ID NO: 14, referred to as 1B1-66/58-77), respectively, of SEQ ID NO: 5, were found to induce a proliferative response and IFN- $\gamma$  production in a Chlamydia-specific T cell line used to screen a genomic library of *C. trachomatis* LGV II.

Further studies have identified a *C. trachomatis*-specific T-cell epitope in the ribosomal S13 protein. Employing standard epitope mapping techniques well known in the art, two T-cell epitopes in the ribosomal S13 protein (rS13) were identified with a *Chlamydia*-specific T-cell line from donor CL-8 (T-cell line TCL-8 EB/DC). Fig. 8 illustrates that the first peptide, rS13 1-20 (SEQ ID NO: 106), is 100% identical with the corresponding *C. pneumoniae* sequence, explaining the cross-reactivity of the T-cell line to recombinant *C. trachomatis*- and *C. pneumoniae*-rS13. The response to the second peptide

rS13 56-75 (SEQ ID NO: 108) is *C. trachomatis*-specific, indicating that the rS13 response in this healthy asymptomatic donor was elicited by exposure to *C. trachomatis* and not to *C. pneumoniae*, or any other microbial infection.

As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMBC. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating  $2.5 \times 10^4$  TCP-21 T-cells in the presence of  $1 \times 10^4$  monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMBC protein (0.1  $\mu$ g/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

To further define the epitope described above, an additional T-cell line, TCT-3, was used in epitope mapping experiments. The immunoassays were performed as described above, except that only peptides from *C. trachomatis* were tested. The T-cells gave a proliferative response to two peptides, CT-OMCB #152-171 and CT-OMCB #157-176 (SEQ ID NO: 246 and 247, respectively), thereby defining an additional immunogenic epitope in the cysteine rich outer membrane protein of *C. trachomatis*.

Clone 14H1-4, (SEQ ID NO: 56, with the corresponding full-length amino acid sequence provided in SEQ ID NO: 92), was identified using the TCT-3 cell line in the CD4 T-cell expression cloning system previously described, and was shown to contain a complete ORF for the, thiol specific antioxidant gene (CT603), referred to as TSA. Epitope

mapping immunoassays were performed, as described above, to further define the epitope. The TCT-3 T-cells line exhibited a strong proliferative response to the overlapping peptides CT-TSA #96-115, CT-TSA #101-120 and CT-TSA #106-125 (SEQ ID NO: 254-256, respectively) demonstrating an immunoreactive epitope in the thiol specific antioxidant gene of *C. trachomatis* serovar LGVII.

### EXAMPLE 3

#### PREPARATION OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using FMOC chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugating or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

## EXAMPLE 4

ISOLATION AND CHARACTERIZATION OF DNA SEQUENCES ENCODING  
CHLAMYDIA ANTIGENS USING RETROVIRAL EXPRESSION VECTOR SYSTEMS  
AND SUBSEQUENT IMMUNOLOGICAL ANALYSIS

A genomic library of *Chlamydia trachomatis* LGV II was constructed by limited digests using BamHI, BglII, BstYI and MboI restriction enzymes. The restriction digest fragments were subsequently ligated into the BamHI site of the retroviral vectors pBIB-KS1,2,3. This vector set was modified to contain a Kosak translation initiation site and stop codons in order to allow expression of proteins from short DNA genomic fragments, as shown in Fig. 2. DNA pools of 80 clones were prepared and transfected into the retroviral packaging line Phoenix-Ampho, as described in Pear, W.S., Scott, M.L. and Nolan, G.P., Generation of High Titre, Helper-free Retroviruses by Transient Transfection. Methods in Molecular Medicine: Gene Therapy Protocols, Humana Press, Totowa, NJ, pp. 41-57. The *Chlamydia* library in retroviral form was then transduced into H2-Ld expressing P815 cells, which were then used as target cells to stimulate an antigen specific T-cell line.

A *Chlamydia*-specific, murine H2<sup>d</sup> restricted CD8+ T-cell line was expanded in culture by repeated rounds of stimulation with irradiated *C. trachomatis*-infected J774 cells and irradiated syngeneic spleen cells, as described by Starnbach, M., in *J. Immunol.*, 153:5183, 1994. This *Chlamydia*-specific T-cell line was used to screen the above *Chlamydia* genomic library expressed by the retrovirally-transduced P815 cells. Positive DNA pools were identified by detection of IFN- $\gamma$  production using Elispot analysis (SEE Lalvani et al., *J. Experimental Medicine* 186:859-865, 1997).

Two positive pools, referred to as 2C7 and 2E10, were identified by IFN- $\gamma$  Elispot assays. Stable transductants of P815 cells from pool 2C7 were cloned by limiting dilution and individual clones were selected based upon their capacity to elicit IFN- $\gamma$  production from the *Chlamydia*-specific CTL line. From this screening process, four positive clones were selected, referred to as 2C7-8, 2C7-9, 2C7-19 and 2C7-21. Similarly, the positive pool 2E10 was further screened, resulting in an additional positive clone, which

contains three inserts. The three inserts are fragments of the CT016, tRNA syntase and clpX genes (SEQ ID NO: 268-270, respectively).

Transgenic DNA from these four positive 2C7.8 clones were PCR amplified using pBIB-KS specific primers to selectively amplify the *Chlamydia* DNA insert. Amplified inserts were gel purified and sequenced. One immunoreactive clone, 2C7-8 (SEQ ID NO: 15, with the predicted amino acid sequence provided in SEQ ID NO: 32), is a 160 bp fragment with homology to nucleotides 597304-597145 of *Chlamydia trachomatis*, serovar D (NCBI, BLASTN search; SEQ ID NO: 33, with the predicted amino acid sequence provided in SEQ ID NO: 34). The sequence of clone 2C7-8 maps within two putative open reading frames from the region of high homology described immediately above, and in particular, one of these putative open reading frames, consisting of a 298 amino acid fragment (SEQ ID NO: 16, with the predicted amino acid sequence provided in SEQ ID NO: 17), was demonstrated to exhibit immunological activity.

Full-length cloning of the 298 amino acid fragment (referred to as CT529 and/or the Cap1 gene) from serovar L2 was obtained by PCR amplification using 5'-ttttgaagcaggtaggtgaatag (forward) (SEQ ID NO: 159) and 5'-ttaagaaattaaaaatccctta (reverse) (SEQ ID NO: 160) primers, using purified *C. trachomatis* L2 genomic DNA as template. This PCR product was gel-purified, cloned into pCRBlunt (Invitrogen, Carlsbad, CA) for sequencing, and then subcloned into the EcoRI site of pBIB-KMS, a derivative of pBIB-KS for expression. The *Chlamydia pneumoniae* homologue of CT529 is provided in SEQ ID NO: 291, with the corresponding amino acid sequence provided in SEQ ID NO: 292.

Full-length DNA encoding various CT529 serovars were amplified by PCR from bacterial lysates containing  $10^5$  IFU, essentially as described (Denamur, E., C. Sayada, A. Souriau, J. Orfila, A. Rodolakis and J. Elion. 1991. J. Gen. Microbiol. 137: 2525). The following serovars were amplified as described: Ba (SEQ ID NO: 134, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 135); E (BOUR) and E (MTW447) (SEQ ID NO: 122, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 123); F (NI1) (SEQ ID NO: 128, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 129); G; (SEQ ID NO: 126, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 127); Ia (SEQ ID

NO: 124, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 125); L1 (SEQ ID NO: 130, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 131); L3 (SEQ ID NO: 132, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 133); I (SEQ ID NO: 263, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 264); K (SEQ ID NO: 265, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 266); and MoPn (SEQ ID NO: 136, with the corresponding predicted amino acid sequence provided in SEQ ID NO: 137). PCR reactions were performed with Advantage Genomic PCR Kit (Clontech, Palo Alto, CA) using primers specific for serovar L2 DNA (external to the ORF). Primers sequences were 5'-ggtataatatctctaaatttg (forward-SEQ ID NO: 161) and 5'-agataaaaaaggctgttc' (reverse-SEQ ID NO: 162) except for MoPn which required 5'-tttgaaggcaggttagtgaatatg (forward-SEQ ID NO: 163) and 5'-tttacaataagaaaagctaagcactttgt (reverse-SEQ ID NO: 164). PCR amplified DNA was purified with QIAquick PCR purification kit (Qiagen, Valencia, CA) and cloned in pCR2.1 (Invitrogen, Carlsbad, CA) for sequencing.

Sequencing of DNA derived from PCR amplified inserts of immunoreactive clones was done on an automated sequencer (ABI 377) using both a pBIB-KS specific forward primer 5'-ccctcacacagtccgtgcac (SEQ ID NO: 165) and a reverse primer 3'-gtttccggccctcacattg (SEQ ID NO: 166). PCRBlunt cloned DNA coding for CT529 serovar L2 and pCR2.1 cloned DNA coding for CT529 serovar Ba, E (BOUR), E (MTW447), F (NI1), G, Ia, K, L1, L3 and MoPn were sequenced using T7 promoter primer and universal M13 forward and M13 reverse primers.

To determine if these two putative open reading frames (SEQ ID NO: 16 and 20) encoded a protein with an associated immunological function, overlapping peptides (17-20 amino acid lengths) spanning the lengths of the two open reading frames were synthesized, as described in Example 3. A standard chromium release assay was utilized to determine the per cent specific lysis of peptide-pulsed H2<sup>d</sup> restricted target cells. In this assay, aliquots of P815 cells (H2<sup>d</sup>) were labeled at 37° C for one hour with 100 µCi of <sup>51</sup>Cr in the presence or absence of 1 µg/ml of the indicated peptides. Following this incubation, labeled P815 cells were washed to remove excess <sup>51</sup>Cr and peptide, and subsequently plated

in duplicate in microculture plates at a concentration of 1,000 cells/well. Effector CTL (*Chlamydia*-specific CD8 T cells) were added at the indicated effector:target ratios. Following a 4 hour incubation, supernatants were harvested and measured by gamma-counter for release of  $^{51}\text{Cr}$  into the supernatant. Two overlapping peptides from the 298 amino acid open reading frame did specifically stimulate the CTL line. The peptides represented in SEQ ID NO: 138-156 were synthesized, representing the translation of the L2 homologue of the serovar D open reading frame for CT529 (Cap1 gene) and 216 amino acid open reading frame. As shown in Fig. 3, peptides CtC7.8-12 (SEQ ID NO: 18, also referred to as Cap1#132-147, SEQ ID NO: 139) and CtC7.8-13 (SEQ ID NO: 19, also referred to as Cap1#138-155, SEQ ID NO: 140) were able to elicit 38 to 52% specific lysis, respectively, at an effector to target ratio of 10:1. Notably, the overlap between these two peptides contained a predicted H2<sup>d</sup> (K<sup>d</sup> and L<sup>d</sup>) binding peptide. A 10 amino acid peptide was synthesized to correspond to this overlapping sequence (SEQ ID NO: 31) and was found to generate a strong immune response from the anti-*Chlamydia* CTL line by elispot assay. Significantly, a search of the most recent Genbank database revealed no proteins have previously been described for this gene. Therefore, the putative open reading frame encoding clone 2C7-8 (SEQ ID NO: 15) defines a gene which encompasses an antigen from *Chlamydia* capable of stimulating antigen-specific CD8+ T-cells in a MHC-I restricted manner, demonstrating this antigen could be used to develop a vaccine against *Chlamydia*.

To confirm these results and to further map the epitope, truncated peptides (SEQ ID NO: 138-156) were made and tested for recognition by the T-cells in an IFN- $\gamma$  ELISPOT assay. Truncations of either Ser139 (Cap1#140-147, SEQ ID NO: 146) or Leu147 (Cap1#138-146, SEQ ID NO: 147) abrogate T-cell recognition. These results indicate that the 9-mer peptide Cap1#139-147 (SFIGGITYL, SEQ ID NO: 145) is the minimal epitope recognized by the *Chlamydia*-specific T-cells.

Sequence alignments of Cap1 (CT529) from selected serovars of *C. trachomatis* (SEQ ID NO: 121, 123, 125, 127, 129, 131, 133, 135, 137 and 139) shows one of the amino acid differences is found in position 2 of the proposed epitope. The homologous serovar D peptide is SIIGGITYL (SEQ ID NO: 168). The ability of SFIGGITYL and SIIGGITYL to target cells for recognition by the *Chlamydia* specific T-cells was compared.

Serial dilutions of each peptide were incubated with P815 cells and tested for recognition by the T-cells in a  $^{51}\text{Cr}$  release assay, as described above. The *Chlamydia*-specific T-cells recognize the serovar L2 peptide at a minimum concentration of 1 nM and the serovar D peptide at a minimum concentration of 10 nM.

Further studies have shown that a Cap1#139-147-specific T-cell clone recognizes *C. trachomatis* infected cells. To confirm that Cap1<sub>139-147</sub> is presented on the surface of *Chlamydia* infected cells, Balb-3T3 (H-2<sup>d</sup>) cells were infected with *C. trachomatis* serovar L2 and tested to determine whether these cells are recognized by a CD8+ T-cell clone specific for Cap1#139-147 epitope (SEQ ID NO: 145). The T-cell clone specific for Cap1#139-147 epitope was obtained by limiting dilution of the line 69 T-cells. The T-cell clone specifically recognized the *Chlamydia* infected cells. In these experiments, target cells were *C. trachomatis* infected (positive control) or uninfected Balb/3T3 cells, showing 45%, 36% and 30% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively; or Cap1#139-147 epitope (SEQ ID NO: 145) coated, or untreated P815 cells, showing 83%, 75% and 58% specific lysis at 30:1, 10:1 and 3:1 effector to target ratios, respectively (negative controls having less than 5% lysis in all cases). This data suggests that the epitope is presented during infection.

In vivo studies show Cap1#139-147 epitope-specific T-cells are primed during murine infection with *C. trachomatis*. To determine if infection with *C. trachomatis* primes a Cap1#139-147 epitope-specific T-cell response, mice were infected i.p. with  $10^8$  IFU of *C. trachomatis* serovar L2. Two weeks after infection, the mice were sacrificed and spleen cells were stimulated on irradiated syngeneic spleen cells pulsed with Cap1#139-147 epitope peptide. After 5 days of stimulation, the cultures were used in a standard  $^{51}\text{Cr}$  release assay to determine if there were Cap1#139-147 epitope-specific T-cells present in the culture. Specifically, spleen cells from a *C. trachomatis* serovar L2 immunized mouse or a control mouse injected with PBS after a 5 days culture with Cap1#139-147 peptide-coated syngeneic spleen cells and CD8+ T-cells able to specifically recognize Cap1#139-147 epitope gave 73%, 60% and 32% specific lysis at a 30:1, 10:1 and 3:1 effector to target ratios, respectively. The control mice had a percent lysis of approximately 10% at a 30:1 effector to target ratio, and steadily declining with lowering E:T ratios. Target cells were Cap1#139-147 peptide-

coated, or untreated P815 cells. These data suggest that Cap1#139-147 peptide-specific T-cells are primed during murine infection with *C. trachomatis*.

#### EXAMPLE 5

##### GENERATION OF ANTIBODY AND T-CELL RESPONSES IN MICE IMMUNIZED WITH CHLAMYDIA ANTIGENS

Immunogenicity studies were conducted to determine the antibody and CD4+ T cell responses in mice immunized with either purified SWIB or S13 proteins formulated with Montanide adjuvant, or DNA-based immunizations with pcDNA-3 expression vectors containing the DNA sequences for SWIB or S13. SWIB is also referred to as clone 1-B1-66 (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5), and S13 ribosomal protein is also referred to as clone 10-C10-31 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12). In the first experiment, groups of three C57BL/6 mice were immunized twice and monitored for antibody and CD4+ T-cell responses. DNA immunizations were intradermal at the base of the tail and polypeptide immunizations were administered by subcutaneous route. Results from standard <sup>3</sup>H-incorporation assays of spleen cells from immunized mice shows a strong proliferative response from the group immunized with purified recombinant SWIB polypeptide (SEQ ID NO: 5). Further analysis by cytokine induction assays, as previously described, demonstrated that the group immunized with SWIB polypeptide produced a measurable IFN- $\gamma$  and IL-4 response. Subsequent ELISA-based assays to determine the predominant antibody isotype response in the experimental group immunized with the SWIB polypeptide were performed. Fig. 4 illustrates the SWIB-immunized group gave a humoral response that was predominantly IgG1.

In a second experiment, C3H mice were immunized three times with 10  $\mu$ g purified SWIB protein (also referred to as clone 1-B1-66, SEQ ID NO: 5) formulated in either PBS or Montanide at three week intervals and harvested two weeks after the third immunization. Antibody titers directed against the SWIB protein were determined by

standard ELISA-based techniques well known in the art, demonstrating the SWIB protein formulated with Montanide adjuvant induced a strong humoral immune response. T-cell proliferative responses were determined by a XTT-based assay (Scudiero, et al, *Cancer Research*, 1988, 48:4827). As shown in Fig. 5, splenocytes from mice immunized with the SWIB polypeptide plus Montanide elicited an antigen specific proliferative response. In addition, the capacity of splenocytes from immunized animals to secrete IFN- $\gamma$  in response to soluble recombinant SWIB polypeptide was determined using the cytokine induction assay previously described. The splenocytes from all animals in the group immunized with SWIB polypeptide formulated with montanide adjuvant secreted IFN- $\gamma$  in response to exposure to the SWIB Chlamydia antigen, demonstrating an *Chlamydia*-specific immune response.

In a further experiment, C3H mice were immunized at three separate time points at the base of the tail with 10  $\mu$ g of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) formulated with the SBAS2 adjuvant (SmithKline Beecham, London, England). Antigen-specific antibody titers were measured by ELISA, showing both polypeptides induced a strong IgG response, ranging in titers from  $1 \times 10^4$  to  $1 \times 10^5$ . The IgG1 and IgG2a components of this response were present in fairly equal amounts. Antigen-specific T-cell proliferative responses, determined by standard  $^3$ H-incorporation assays on spleen cells isolated from immunized mice, were quite strong for SWIB (50,000 cpm above the negative control) and even stronger for s13 (100,000 cpm above the negative control). The IFN $\gamma$  production was assayed by standard ELISA techniques from supernatant from the proliferating culture. *In vitro* restimulation of the culture with S13 protein induced high levels of IFN $\gamma$  production, approximately 25 ng/ml versus 2 ng/ml for the negative control. Restimulation with the SWIB protein also induced IFN $\gamma$ , although to a lesser extent.

In a related experiment, C3H mice were immunized at three separate time points with 10  $\mu$ g of purified SWIB or S13 protein (*C. trachomatis*, SWIB protein, clone 1-B1-66, SEQ ID NO: 5, and S13 protein, clone 10-C10-31, SEQ ID NO: 4) mixed with 10  $\mu$ g of Cholera Toxin. Mucosal immunization was through intranasal inoculation. Antigen-specific antibody responses were determined by standard ELISA techniques. Antigen-specific IgG antibodies were present in the blood of SWIB-immunized mice, with titers

ranging from  $1 \times 10^{-3}$  to  $1 \times 10^{-4}$ , but non-detectable in the S13-immunized animals. Antigen-specific T-cell responses from isolated splenocytes, as measured by IFN $\gamma$  production, gave similar results to those described immediately above for systemic immunization.

An animal study was conducted to determine the immunogenicity of the CT529 serovar LGVII CTL epitope, defined by the CT529 10mer consensus peptide (CSFIGGITYL – SEQ ID NO: 31), which was identified as an H2-Kd restricted CTL epitope. BALB/c mice (3 mice per group) were immunized three times with 25  $\mu$ g of peptide combined with various adjuvants. The peptide was administered systemically at the base of the tail in either SKB Adjuvant System SBAS-2", SBAS-7 (SmithKline Beecham, London, England) or Montanide. The peptide was also administered intranasally mixed with 10ug of Cholera Toxin (CT). Naive mice were used as a control. Four weeks after the 3rd immunization, spleen cells were restimulated with LPS- blasts pulsed with 10ug/ml CT529 10mer consensus peptide at three different effector to LPS- blasts ratios : 6, 1.5 and 0.4 at  $1 \times 10^6$  cell/ml. After 2 restimulations, effector cells were tested for their ability to lyse peptide pulsed P815 cells using a standard chromium release assay. A non-relevant peptide from chicken egg ovalbumin was used as a negative control. The results demonstrate that a significant immune response was elicited towards the CT529 10mer consensus peptide and that antigen-specific T-cells capable of lysing peptide-pulsed targets were elicited in response to immunization with the peptide. Specifically, antigen-specific lytic activities were found in the SBAS-7 and CT adjuvanted group while Montanide and SBAS-2" failed to adjuvant the CTL epitope immunization.

#### EXAMPLE 6

#### EXPRESSION AND CHARACTERIZATION OF *CHLAMYDIA PNEUMONIAE* GENES

The human T-cell line, TCL-8, described in Example 1, recognizes *Chlamydia trachomatis* as well as *Chlamydia pneumoniae* infected monocyte-derived dendritic cells, suggesting *Chlamydia trachomatis* and *pneumoniae* may encode cross-reactive T-cell epitopes. To isolate the *Chlamydia pneumoniae* genes homologous to *Chlamydia trachomatis* LGV II

clones 1B1-66, also referred to as SWIB (SEQ ID NO: 1) and clone 10C10-31, also referred to as S13 ribosomal protein (SEQ ID NO: 4), HeLa 229 cells were infected with *C. pneumonia* strain TWAR (CDC/CWL-029). After three days incubation, the *C. pneumonia*-infected HeLa cells were harvested, washed and resuspended in 200 µl water and heated in a boiling water bath for 20 minutes. Ten microliters of the disrupted cell suspension was used as the PCR template.

*C. pneumonia* specific primers were designed for clones 1B1-66 and 10C10-31 such that the 5' end had a 6X-Histidine tag and a Nde I site inserted, and the 3' end had a stop codon and a BamHI site included (Fig. 6). The PCR products were amplified and sequenced by standard techniques well known in the art. The *C. pneumonia*-specific PCR products were cloned into expression vector pET17B (Novagen, Madison, WI) and transfected into *E. coli* BL21 pLysS for expression and subsequent purification utilizing the histidine-nickel chromatographic methodology provided by Novagen. Two proteins from *C. pneumonia* were thus generated, a 10-11 kDa protein referred to as CpSWIB (SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively), a 15 kDa protein referred to as CpS13 (SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 30 and 91, respectively).

#### EXAMPLE 7

##### INDUCTION OF T CELL PROLIFERATION AND INTERFERON- $\gamma$ PRODUCTION BY CHLAMYDIA PNEUMONIAE ANTIGENS

The ability of recombinant *Chlamydia pneumoniae* antigens to induce T cell proliferation and interferon- $\gamma$  production is determined as follows.

Proteins are induced by IPTG and purified by Ni-NTA agarose affinity chromatography (Webb et al., *J. Immunology* 157:5034-5041, 1996). The purified polypeptides are then screened for the ability to induce T-cell proliferation in PBMC preparations. PBMCs from *C. pneumoniae* patients as well as from normal donors whose T-

cells are known to proliferate in response to *Chlamydia* antigens, are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified polypeptides are added in duplicate at concentrations of 0.5 to 10 µg/mL. After six days of culture in 96-well round-bottom plates in a volume of 200 µl, 50 µl of medium is removed from each well for determination of IFN-γ levels, as described below. The plates are then pulsed with 1 µCi/well of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

IFN-γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates are coated with a mouse monoclonal antibody directed to human IFN-γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells are then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates are washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates are incubated overnight at room temperature. The plates are again washed and a polyclonal rabbit anti-human IFN-γ serum diluted 1:3000 in PBS/10% normal goat serum is added to each well. The plates are then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) is added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates are washed and TMB substrate added. The reaction is stopped after 20 min with 1 N sulfuric acid. Optical density is determined at 450 nm using 570 nm as a reference wavelength. Fractions that result in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, are considered positive.

A human anti-*Chlamydia* T-cell line (TCL-8) capable of cross-reacting to *C. trachomatis* and *C. pneumonia* was used to determine whether the expressed proteins described in the example above, (i.e., CpSWIB, SEQ ID NO: 27, and SEQ ID NO: 78 having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID NO: 28, respectively, and the 15 kDa protein referred to as CpS13 SEQ ID NO: 29, and SEQ ID NO: 77, having a 6X His tag, with the corresponding amino acid sequence provided in SEQ ID

NO: 30 and 91, respectively), possessed T-cell epitopes common to both *C. trachomatis* and *C. pneumonia*. Briefly, *E. coli* expressing *Chlamydial* proteins were titered on  $1 \times 10^4$  monocyte-derived dendritic cells. After two hours, the dendritic cells cultures were washed and  $2.5 \times 10^4$  T cells (TCL-8) added and allowed to incubate for an additional 72 hours. The amount of INF- $\gamma$  in the culture supernatant was then determined by ELISA. As shown in Figs. 7A and 7B, the TCL-8 T-cell line specifically recognized the S13 ribosomal protein from both *C. trachomatis* and *C. pneumonia* as demonstrated by the antigen-specific induction of IFN- $\gamma$ , whereas only the SWIB protein from *C. trachomatis* was recognized by the T-cell line. To validate these results, the T cell epitope of *C. trachomatis* SWIB was identified by epitope mapping using target cells pulsed with a series of overlapping peptides and the T-cell line TCL-8. 3H-thymidine incorporation assays demonstrated that the peptide, referred to as C.t.SWIB 52-67, of SEQ ID NO: 39 gave the strongest proliferation of the TCL-8 line. The homologous peptides corresponding to the SWIB of *C. pneumoniae* sequence (SEQ ID NO: 40), the topoisomerase-SWIB fusion of *C. pneumoniae* (SEQ ID NO: 43) and *C. trachomatis* (SEQ ID NO: 42) as well as the human SWI domain (SEQ ID NO: 41) were synthesized and tested in the above assay. The T-cell line TCL-8 only recognized the *C. trachomatis* peptide of SEQ ID NO: 39 and not the corresponding *C. pneumoniae* peptide (SEQ ID NO: 40), or the other corresponding peptides described above (SEQ ID NO: 41-43).

Chlamydia-specific T cell lines were generated from donor CP-21 with a positive serum titer against *C. pneumoniae* by stimulating donor PBMC with either *C. trachomatis* or *C. pneumoniae*-infected monocyte-derived dendritic cells, respectively. T-cells generated against *C. pneumoniae* responded to recombinant *C. pneumoniae*-SWIB but not *C. trachomatis*-SWIB, whereas the T-cell line generated against *C. trachomatis* did not respond to either *C. trachomatis*- or *C. pneumoniae*-SWIB (see Fig. 9). The *C. pneumoniae*-SWIB specific immune response of donor CP-21 confirms the *C. pneumoniae* infection and indicates the elicitation of *C. pneumoniae*-SWIB specific T-cells during *in vivo* *C. pneumoniae* infection.

Epitope mapping of the T-cell response to *C. pneumoniae*-SWIB has shown that Cp-SWIB-specific T-cells responded to the overlapping peptides Cp-SWIB 32-51 (SEQ

ID NO: 101) and Cp-SWIB 37-56 (SEQ ID NO: 102), indicating a *C. pneumoniae*-SWIB-specific T-cell epitope Cp-SWIB 37-51 (SEQ ID NO: 100).

In additional experiments, T-cell lines were generated from donor CP1, also a *C. pneumoniae* seropositive donor, by stimulating PBMC with non-infectious elementary bodies from *C. trachomatis* and *C. pneumoniae*, respectively. In particular, proliferative responses were determined by stimulating  $2.5 \times 10^4$  T-cells in the presence of  $1 \times 10^4$  monocyte-derived dendritic cells and non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or either recombinant *C. trachomatis* or *C. pneumoniae* SWIB protein. The T-cell response against SWIB resembled the data obtained with T-cell lines from CP-21 in that *C. pneumoniae*-SWIB, but not *C. trachomatis*-SWIB elicited a response by the *C. pneumoniae* T-cell line. In addition, the *C. trachomatis* T-cell line did not proliferate in response to either *C. trachomatis* or *C. pneumoniae* SWIB, though it did proliferate in response to both CT and CP elementary bodies. As described in Example 1, Clone 11-C12-91 (SEQ ID NO: 63), identified using the TCP-21 cell line, has a 269 bp insert that is part of the OMP2 gene (CT443) and shares homology with the 60 kDa cysteine rich outer membrane protein of *C. pneumoniae*, referred to as OMBC. To further define the reactive epitope(s), epitope mapping was performed using a series of overlapping peptides and the immunoassay previously described. Briefly, proliferative responses were determined by stimulating  $2.5 \times 10^4$  TCP-21 T-cells in the presence of  $1 \times 10^4$  monocyte-derived dendritic cells with either non-infectious elementary bodies derived from *C. trachomatis* and *C. pneumoniae*, or peptides derived from the protein sequence of *C. trachomatis* or *C. pneumoniae* OMBC protein (0.1 µg/ml). The TCP-21 T-cells responded to epitopes CT-OMCB #167-186, CT-OMCB #171-190, CT-OMCB #171-186, and to a lesser extent, CT-OMCB #175-186 (SEQ ID NO: 249-252, respectively). Notably, the TCP-21 T-cell line also gave a proliferative response to the homologous *C. pneumoniae* peptide CP-OMCB #171-186 (SEQ ID NO: 253), which was equal to or greater than the response to the *C. trachomatis* peptides. The amino acid substitutions in position two (i.e., Asp for Glu) and position four (i.e., Cys for Ser) did not alter the proliferative response of the T-cells and therefore demonstrating this epitope to be a cross-reactive epitope between *C. trachomatis* and *C. pneumoniae*.

## EXAMPLE 8

IMMUNE RESPONSES OF HUMAN PBMC AND T-CELL LINES AGAINST  
CHLAMYDIA ANTIGENS

The examples provided herein suggest that there is a population of healthy donors among the general population that have been infected with *C. trachomatis* and generated a protective immune response controlling the *C. trachomatis* infection. These donors remained clinically asymptomatic and seronegative for *C. trachomatis*. To characterize the immune responses of normal donors against *chlamydial* antigens which had been identified by CD4 expression cloning, PBMC obtained from 12 healthy donors were tested against a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and *C. trachomatis*-, *C. pneumoniae*-S13. The data are summarized in Table I below. All donors were seronegative for *C. trachomatis*, whereas 6/12 had a positive *C. pneumoniae* titer. Using a stimulation index of >4 as a positive response, 11/12 of the subjects responded to *C. trachomatis* elementary bodies and 12/12 responded to *C. pneumoniae* elementary bodies. One donor, AD104, responded to recombinant *C. pneumoniae*-S13 protein, but not to recombinant *C. trachomatis*-S13 protein, indicating a *C. pneumoniae*-specific response. Three out of 12 donors had a *C. trachomatis*-SWIB, but not a *C. pneumoniae*-SWIB specific response, confirming a *C. trachomatis* infection. *C. trachomatis* and *C. pneumoniae*- S13 elicited a response in 8/12 donors suggesting a chlamydial infection. These data demonstrate the ability of SWIB and S13 to elicit a T-cell response in PBMC of normal study subjects.

Table I.

Immune response of normal study subjects against <i>Chlamydia</i>										
conr	Sex	<i>Chlamydia</i> IgGtiter	CT EB	CP EB	CT Swib	CP Swib	CT S13	CP S13	CT lpdA	CT TSA
D100	male	negative	++	+++	+	-	++	++	-	nt
D104	female	negative	+++	++	-	-	-	++	-	nt
D108	male	CP 1:256	++	++	+	+/-	+	+	+	nt
D112	female	negative	++	++	+	-	+	-	+/-	nt
D120	male	negative	-	+	-	-	-	-	-	nt
D124	female	CP 1:128	++	++	-	-	-	-	-	nt
D128	male	CP 1:512	+	++	-	-	++	+	++	-
D132	female	negative	++	++	-	-	+	+	-	-
D136	female	CP 1:128	+	++	-	-	+/-	-	-	-
D140	male	CP 1:256	++	++	-	-	+	+	-	-
D142	female	CP 1:512	++	++	-	-	+	+	+	-
D146	female	negative	++	++	-	-	++	+	+	-

CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein. Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating  $3 \times 10^5$  PBMC with  $1 \times 10^4$  monocyte-derived dendritic cells pre-incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a  $^3\text{H}$ -thymidine pulse for the last 18h.

SI: Stimulation index

+/-:	SI ~	4
+:	SI >	4
++:	SI	10-30
+++:	SI >	30

In a first series of experiments, T-cell lines were generated from a healthy female individual (CT-10) with a history of genital exposure to *C. trachomatis* by stimulating T-cells with *C. trachomatis* LGV II elementary bodies as previously described. Although the study subject was exposed to *C. trachomatis*, she did not seroconvert and did not develop clinical symptoms, suggesting donor CT-10 may have developed a protective immune response against *C. trachomatis*. As shown in Fig. 10, a primary *Chlamydia*-specific T-cell line derived from donor CT-10 responded to *C. trachomatis*-SWIB, but not *C. pneumoniae*-SWIB recombinant proteins, confirming the exposure of CT-10 to *C. trachomatis*. Epitope mapping of the T-cell response to *C. trachomatis*-SWIB showed that this donor responded to the same epitope Ct-SWIB 52-67 (SEQ ID NO: 39) as T-cell line TCL-8, as shown in Fig. 11.

Additional T-cell lines were generated as described above for various *C. trachomatis* patients. A summary of the patients' clinical profile and proliferative responses to various *C. trachomatis* and *C. pneumoniae* elementary bodies and recombinant proteins are summarized in Table II .

<b>Proliferative response of <i>C. trachomatis</i> patients</b>											
Patients	Clinical manifestation	IgG titer	CT	CP	CT	CP	CT	CP	CT	lpdA	CT
			Table II.	EB	Swib	Swib	S13	S13	TSA		
CT-1	NGU	<b>negative</b>	+	+	-	-	++	++	++	++	+
CT-2	NGU	<b>negative</b>	++	++	-	-	+	+/-	-	-	-
CT-3	asymptomatic shed Eb Dx was HPV	<b>Ct 1:512 Cp 1:1024 Cps 1:256</b>	+	+	-	-	+	-	+	-	-
CT-4	asymptomatic shed Eb	<b>Ct 1:1024</b>	+	+	-	-	-	-	-	-	-
CT-5	BV	<b>Ct 1:256 Cp 1:256</b>	++	++	-	-	+	-	-	-	-
CT-6	perinial rash discharge	<b>Cp 1:1024</b>	+	+	-	-	-	-	-	-	-
CT-7	BV genital ulcer	<b>Ct 1:512 Cp 1:1024</b>	+	+	-	-	+	+	+	-	-
CT-8	Not known	<b>Not tested</b>	++	++	-	-	-	-	-	-	-
CT-9	asymptomatic	<b>Ct 1:128 Cp 1:128</b>	+++	++	-	-	++	+	+	-	-
CT-10	Itch mild vulvar	<b>negative</b>	++	++	-	-	-	-	-	-	-
CT-11	BV, abnormal pap	<b>Ct 1: 512</b>	+++	+++	-	-	+++	+/-	++	+	+
CT-12	asymptomatic	<b>Cp 1: 512</b>	++	++	-	-	++	+	+	-	-

NGU= Non-Gonococcal Urethritis; BV= Bacterial Vaginosis; CT= *Chlamydia trachomatis*; CP= *Chlamydia pneumoniae*; EB= *Chlamydia* elementary bodies; Swib= recombinant *Chlamydia* Swib protein; S13= recombinant *Chlamydia* S13 protein; lpdA= recombinant *Chlamydia* lpdA protein; TSA= recombinant *Chlamydia* TSA protein

Values represent results from standard proliferation assays. Proliferative responses were determined by stimulating  $3 \times 10^5$  PBMC with  $1 \times 10^4$  monocyte-derived dendritic cells pre-

incubated with the respective recombinant antigens or elementary bodies (EB). Assays were harvested after 6 days with a  $^3\text{H}$ -thymidine pulse for the last 18 hours.

SI: Stimulation index

+/-:	SI ~	4
+:	SI >	4
++:	SI	10-30
+++:	SI >	30

Using the panel of asymptomatic (as defined above) study subjects and *C. trachomatis* patients, as summarized in Tables I and II, a comprehensive study of the immune responses of PBMC derived from the two groups was conducted. Briefly, PBMCs from *C. pneumoniae* patients as well as from normal donors are cultured in medium comprising RPMI 1640 supplemented with 10% pooled human serum and 50  $\mu\text{g}/\text{ml}$  gentamicin. Purified polypeptides, a panel of recombinant *chlamydial* antigens including *C. trachomatis*-, *C. pneumoniae*-SWIB and S13, as well as *C. trachomatis* lpdA and TSA are added in duplicate at concentrations of 0.5 to 10  $\mu\text{g}/\text{mL}$ . After six days of culture in 96-well round-bottom plates in a volume of 200  $\mu\text{l}$ , 50  $\mu\text{l}$  of medium is removed from each well for determination of IFN- $\gamma$  levels, as described below. The plates are then pulsed with 1  $\mu\text{Ci}/\text{well}$  of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that result in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone are considered positive.

Proliferative responses to the recombinant *Chlamydiae* antigens demonstrated that the majority of asymptomatic donors and *C. trachomatis* patients recognized the *C. trachomatis* S13 antigen (8/12) and a majority of the *C. trachomatis* patients recognized the *C. pneumonia* S13 antigen (8/12), with 4/12 asymptomatic donors also recognizing the *C. pneumonia* S13 antigen. Also, six out of twelve of the *C. trachomatis* patients and four out of twelve of the asymptomatic donors gave a proliferative response to the lpdA antigen of *C. trachomatis*. These results demonstrate that the *C. trachomatis* and *C. pneumonia* S13 antigen, *C. trachomatis* Swib antigen and the *C. trachomatis* lpdA antigen are recognized by the asymptomatic donors, indicating these antigens were recognized during exposure to *Chlamydia* and an immune response elicited against them. This implies these antigens may

play a role in conferring protective immunity in a human host. In addition, the *C. trachomatis* and *C. pneumonia* S13 antigen is recognized equally well among the *C. trachomatis* patients, therefore indicating there may be epitopes shared between *C. trachomatis* and *C. pneumonia* in the S13 protein. Table III summarizes the results of these studies.

Table III.

Antigen	Normal Donors	C.t. Patients
C.t.-Swib	3/12	0/12
C.p.-Swib	0/12	0/12
C.t.-S13	8/12	8/12
C.p.-S13	4/12	8/12
lpdA	4/12	6/12
TSA	0/12	2/12

A series of studies were initiated to determine the cellular immune response to short-term T-cell lines generated from asymptomatic donors and *C. trachomatis* patients. Cellular immune responses were measured by standard proliferation assays and IFN- $\gamma$ , as described in Example 7. Specifically, the majority of the antigens were in the form of single *E. coli* clones expressing Chlamydial antigens, although some recombinant proteins were also used in the assays. The single *E. coli* clones were titered on  $1 \times 10^4$  monocyte-derived dendritic cells and after two hours, the culture was washed and  $2.5 \times 10^4$  T-cells were added. The assay using the recombinant proteins were performed as previously described. Proliferation was determined after four days with a standard  $^3\text{H}$ -thymidine pulse for the last 18 hours. Induction of IFN- $\gamma$  was determined from culture supernatants harvested after four days using standard ELISA assays, as described above. The results show that all the *C. trachomatis* antigens tested, except for C.T. Swib, elicited a proliferative response from one or more different T-cell lines derived from *C. trachomatis* patients. In addition, proliferative responses were elicited from both the *C. trachomatis* patients and asymptomatic donors for

the following *Chlamydia* genes, CT622, groEL, pmpD, CT610 and rS13.

The 12G3-83 clone also contains sequences to CT734 and CT764 in addition to CT622, and therefore these gene sequence may also have immunoreactive epitopes. Similarly, clone 21G12-60 contains sequences to the hypothetical protein genes CT229 and CT228 in addition to CT875; and 15H2-76 also contains sequences from CT812 and CT088, as well as sharing homology to the sycE gene. Clone 11H3-61 also contains sequences sharing homology to the PGP6-D virulence protein.

Table IV.

Clone	C. t. Antigen (putative*)	TCL from Asymp. Donors	TCL from C. t. Patients	SEQ ID NO::
1B1-66 (E. coli)	Swib	2/2	0/4	5
1B1-66 (protein)	Swib	2/2	0/4	5
12G3-83 (E. coli)	CT622*	2/2	4/4	57
22B3-53 (E. coli)	groEL	1/2	4/4	111
22B3-53 (protein)	groEL	1/2	4/4	111
15H2-76 (E. coli)	PmpD*	1/2	3/4	87
11H3-61 (E. coli)	rL1*	0/2	3/4	60
14H1-4 (E. coli)	TSA	0/2	3/4	56
14H1-4 (protein)	TSA	0/2	3/4	56
11G10-46 (E. coli)	CT610	1/2	1/4	62
10C10-17 (E. coli)	rS13	1/2	1/4	62
10C10-17 (protein)	rS13	1/2	1/4	62
21G12-60 (E. coli)	CT875*	0/2	2/4	110
11H4-32 (E. coli)	dnaK	0/2	2/4	59
21C7-8 (E. coli)	dnaK	0/2	2/4	115
17C10-31 (E. coli)	CT858	0/2	2/4	114

**EXAMPLE 9**

**PROTECTION STUDIES USING CHLAMYDIA ANTIGENS**

Protection studies were conducted in mice to determine whether immunization with chlamydial antigens can impact on the genital tract disease resulting from chlamydial inoculation. Two models were utilized; a model of intravaginal inoculation that uses a human isolate containing a strain of *Chlamydia psittaci* (MTW447), and a model of intrauterine inoculation that involves a human isolate identified as *Chlamydia trachomatis*, serovar F (strain NI1). Both strains induce inflammation in the upper genital tract, which resemble endometritis and salpingitis caused by *Chlamydia trachomatis* in women. In the first experiment, C3H mice (4 mice per group) were immunized three times with 100 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5). Inoculations were at the base of the tail for systemic immunization. Two weeks after the last immunization, animals were progesterone treated and infected, either thru the vagina or by injection of the inoculum in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored (from + for very mild, to +++++ for very severe). Scores attributed to each single oviduct/ovary were summed and divided by the number of organs examined to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control-immunized animals receiving empty vector showed consistent inflammation with an ovary/oviduct mean inflammation score of 6.12, in contrast to 2.62 for the DNA-immunized group. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary/oviduct mean inflammation score of 8.37, versus 5.00 for the DNA-immunized group. Also, in the later model, vaccinated mice showed no signs of tubal occlusion while negative control vaccinated groups had inflammatory cells in the lumen of the oviduct.

In a second experiment, C3H mice (4 mice per group) were immunized three times with 50 µg of pcDNA-3 expression vector containing *C. trachomatis* SWIB DNA (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5) encapsulated in Poly Lactide co-Glycolide microspheres (PLG); immunizations were made

intra-peritoneally. Two weeks after the last immunization, animal were progesterone treated and infected by inoculation of *C. psittaci* in the vagina. Two weeks after infection, mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. Inflammation level was scored as previously described. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean of inflammation for the group. Negative control-immunized animals receiving PLG-encapsulated empty vector showed consistent infammtion with an ovary /oviduct mean inflammation score of 7.28, versus 5.71 for the PLG-encapsulated DNA immunized group. Inflammation in the peritoneum was 1.75 for the vaccinated group versus 3. 75 for the control.

In a third experiment, C3H mice (4 per group) were immunized three times with 10 µg of purified recombinant protein, either SWIB (SEQ ID NO: 1, with the corresponding amino acid sequence provided in SEQ ID NO: 5, or S13 (SEQ ID NO: 4, with the corresponding amino acid sequence provided in SEQ ID NO: 12) mixed with Cholera Toxin (CT); the preparation was administered intranasally upon anaesthesia in a 20 uL volume. Two weeks after the last immunization, animal were progesterone treated and infected, either by vaginal inoculation of *C. psittaci* or by injection of *C. trachomatis* serovar F in the uterus. Two weeks after infection, the mice were sacrificed and genital tracts sectioned, stained and examined for histopathology. The degree of inflammation was scored as described above. Scores attributed to each single oviduct /ovary were summed and divided by the number of examined organs to get a mean score of inflammation for the group. In the model of uterine inoculation, negative control- immunized animals receiving cholera toxin alone showed an ovary /oviduct mean inflammation score of 4.25 (only 2 mice analyzed ; 2 other died) versus 5.00 for the s13 plus cholera toxin-immunized group, and 1.00 for the SWIB plus cholera toxin. Untreated infected animals had an ovary /oviduct mean inflammation score of 7. In the model of vaginal inoculation and ascending infection, negative control-immunized mice had an ovary /oviduct mean inflammation score of 7.37 versus 6.75 for the s13 plus cholera toxin-immunized group and 5.37 for the SWIB plus cholera toxin-immunized group. Untreated infected animals had an ovary /oviduct mean inflammation score of 8.

The three experiments described above suggest that SWIB-specific protection is obtainable. This protective effect is more marked in the model of homologous infection but is still present when in a heterologous challenge infection with *C. psittaci*.

Although the present invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, changes and modifications can be carried out without departing from the scope of the invention which is intended to be limited only by the scope of the appended claims.

Claims

1. An isolated polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1, 15, 21-25, 44-64, 66-76, 79-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-290 ; (b) sequences complementary to a sequence of (a); and (c) polynucleotide sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.

2. The polypeptide of claim 1 wherein the polypeptide comprises a sequence selected from the group consisting of SEQ ID NO: 5, 26, 32, 65, 90, 92-98, 103-108, 121, 123, 125, 127, 129, 131, 133, 135, 137, 175-180, 189-196, 264 and 266.

3. An isolated polynucleotide molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1 and 2.

4. A recombinant expression vector comprising a polynucleotide molecule according to claim 3.

5. A host cell transformed with an expression vector according to claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.

7. A fusion protein comprising a polypeptide according to any one of claims 1 and 2.

8. A fusion protein according to claim 7, wherein the fusion protein comprises an expression enhancer that increases expression of the fusion protein in a host cell

transfected with a polynucleotide encoding the fusion protein.

9. A fusion protein according to claim 7, wherein the fusion protein comprises a T helper epitope that is not present within the polypeptide of claim 1.

10. A fusion protein according to claim 7, wherein the fusion protein comprises an affinity tag.

11. An isolated polynucleotide encoding a fusion protein according to claim 7.

12. An isolated monoclonal antibody, or antigen-binding fragment thereof, that specifically binds to a Chlamydia protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence according to claim 1, or a complement of any of the foregoing polynucleotide sequences.

13. A pharmaceutical composition comprising a polypeptide according to claim 1, and a physiologically acceptable carrier.

14. A pharmaceutical composition comprising a polynucleotide molecule according to claim 3 and a physiologically acceptable carrier.

15. A pharmaceutical composition comprising a polypeptide and a physiologically acceptable carrier, wherein the polypeptide is encoded by polynucleotide molecule selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.

16. A pharmaceutical composition comprising a polynucleotide molecule and a physiologically acceptable carrier, wherein the polynucleotide molecule comprises a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.

17. A pharmaceutical composition comprising a physiologically acceptable carrier and at least one component selected from the group consisting of:

- (a) a fusion protein according to claim 7;
- (b) a polynucleotide according to claim 11; and
- (c) an antibody according to claim 12.

18. A vaccine comprising a polypeptide according to claim 1, and an immunostimulant.

19. A vaccine comprising a polynucleotide molecule according to claim 3 and an immunostimulant.

20. A vaccine comprising a polypeptide and an immunostimulant, wherein the polypeptide is encoded by a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291 ; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.

21. A vaccine comprising a DNA molecule and an immunostimulant, wherein the DNA molecule comprises a sequence selected from the group consisting of: (a) sequences recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 122,

124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291; (b) sequences complementary to a sequence of (a); and (c) sequences that hybridize to a sequence of (a) or (b) under moderately stringent conditions.

22. A vaccine comprising an immunostimulant and at least one component selected from the group consisting of:

- (a) a fusion protein according to claim 7;
- (b) a polynucleotide according to claim 11; and
- (c) an antibody according to claim 12.

23. The vaccine of any one of claims 18-22 wherein the immunostimulant is an adjuvant.

24. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 13-17.

25. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 18-22.

26. An isolated polyclonal antibody, or antigen-binding fragment thereof, that specifically binds to a *Chlamydia* protein that comprises an amino acid sequence that is encoded by a polynucleotide sequence according to claim 1, or a complement of any of the foregoing polynucleotide sequences.

27. A method for detecting *Chlamydia* infection in a patient, comprising:

- (a) obtaining a biological sample from the patient;
- (b) contacting the sample with a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence

recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291. (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

- (c) detecting the presence of antibodies that bind to the polypeptide.

28. A method for detecting *Chlamydia* infection in a patient, comprising:

- (a) obtaining a biological sample from the patient;

- (b) contacting the sample with a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

- (c) detecting the presence of antibodies that bind to the fusion protein.

29. The method of any one of claims 27 and 28 wherein the biological sample is selected from the group consisting of whole blood, serum, plasma, saliva, cerebrospinal fluid and urine.

30. A method for detecting *Chlamydia* infection in a biological sample, comprising:

- (a) contacting the sample with at least two oligonucleotide primers in a polymerase chain reaction, wherein at least one of the oligonucleotide primers is specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291; and

(b) detecting in the sample a polynucleotide sequence that amplifies in the presence of the oligonucleotide primers, thereby detecting *Chlamydia* infection.

31. The method of claim 30, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

32. A method for detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the sample with one or more oligonucleotide probes specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291; and

(b) detecting in the sample a polynucleotide sequence that hybridizes to the oligonucleotide probe, thereby detecting *Chlamydia* infection.

33. The method of claim 32 wherein the probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

34. A method for detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291, (ii) sequences complementary to a sequence of (i),

and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) detecting in the sample a polypeptide that binds to the binding agent, thereby detecting *Chlamydia* infection in the biological sample.

35. A method of detecting *Chlamydia* infection in a biological sample, comprising:

(a) contacting the biological sample with a binding agent which is capable of binding to a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291, (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) detecting in the sample a polypeptide that binds to the binding agent, thereby detecting *Chlamydia* infection in the biological sample.

36. The method of any one of claims 34 and 35 wherein the binding agent is a monoclonal antibody.

37. The method of any one of claims 34 and 35 wherein the binding agent is a polyclonal antibody.

38. The method of any one of claims 34 and 35 wherein the biological sample is selected from the group consisting of whole blood, sputum, serum, plasma, saliva, cerebrospinal fluid and urine.

39. A diagnostic kit comprising:

(a) a polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291, (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) a detection reagent.

40. A diagnostic kit comprising:

(a) a fusion protein comprising a polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions; and

(b) a detection reagent.

41. The kit of claims 39 or 40 wherein the polypeptide is immobilized on a solid support.

42. The kit of claims 39 or 40 wherein the detection reagent comprises a reporter group conjugated to a binding agent.

43. The kit of claim 42 wherein the binding agent is selected from the group consisting of anti-immunoglobulins, Protein G, Protein A and lectins.

44. The kit of claim 42 wherein the reporter group is selected from the group consisting of radioisotopes, fluorescent groups, luminescent groups, enzymes, biotin and dye particles.

45. A diagnostic kit comprising at least two oligonucleotide primers, at least one of the oligonucleotide primers being specific for a polynucleotide molecule comprising a polynucleotide sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

46. A diagnostic kit according to claim 43, wherein at least one of the oligonucleotide primers comprises at least about 10 contiguous nucleotides of a sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

47. A diagnostic kit comprising at least one oligonucleotide probe, the oligonucleotide probe being specific for a polynucleotide molecule comprising a sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

48. A kit according to claim 47, wherein the oligonucleotide probe comprises at least about 15 contiguous nucleotides of a polynucleotide sequence of SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291.

49. A diagnostic kit comprising:  
(a) at least one antibody, or antigen-binding fragment thereof,  
according to claim 22; and  
(b) a detection reagent.

50. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

(a) obtaining peripheral blood cells from the patient;

(b) incubating the cells in the presence of at least one polypeptide, the polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said antigen comprises an amino acid sequence encoded by a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions, such that T cells proliferate; and

(c) administering to the patient the proliferated T cells.

51. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

(a) obtaining peripheral blood cells from the patient;

(b) incubating the cells in the presence of at least one polynucleotide, comprises a polynucleotide sequence selected from the group consisting of: (i) a sequence recited in SEQ ID NO: 1-4, 15, 16, 21-25, 27, 29, 33, 44-64, 66-88, 110-119, 120, 122, 124, 126, 128, 130, 132, 134, 136, 169-174, 181-188, 263, 265 and 267-291 (ii) sequences complementary to a sequence of (i), and (c) polynucleotide sequences that hybridize to a sequence of (i) or (ii) under moderately stringent conditions, such that T cells proliferate; and

(c) administering to the patient the proliferated T cells.

52. The method of any one of claims 50 and 51 wherein the step of incubating the T cells is repeated one or more times.

53. The method of any one of claims 50 and 51 wherein step (a) further comprises separating T cells from the peripheral blood cells, and the cells incubated in step (b) are the T cells.

54. The method of any one of claims 50 and 51 wherein step (a) further comprises separating CD4+ cells or CD8+ T cells from the peripheral blood cells, and the cells proliferated in step (b) are CD4+ or CD8+ T cells.

55. The method of any one of claims 50 and 51 wherein step (a) further comprises separating gamma/delta T lymphocytes from the peripheral blood cells, and the cells proliferated in step (b) are gamma/delta T lymphocytes.

56. The method of any one of claims 50 and 51 wherein step (b) further comprises cloning one or more T cells that proliferated in the presence of the polypeptide.

57. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising T cells proliferated in the presence of a polypeptide of claim 1, in combination with a physiologically acceptable carrier.

58. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising T cells proliferated in the presence of a polynucleotide of claim 3, in combination with a physiologically acceptable carrier.

59. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

- (a) incubating antigen presenting cells in the presence of at least one polypeptide of claim 1;
- (b) administering to the patient the incubated antigen presenting cells.

60. A method for treating *Chlamydia* infection in a patient, comprising the steps of:

- (a) introducing at least one polynucleotide of claim 3 into antigen presenting cells;
- (b) administering to the patient the antigen presenting cells.

61. The method of claims 59 or 60 wherein the antigen presenting cells are selected from the group consisting of dendritic cells, macrophage cells, B cells fibroblast cells, monocyte cells, and stem cells.

62. A pharmaceutical composition for the treatment of *Chlamydia* infection in a patient, comprising antigen presenting cells incubated in the presence of a polypeptide of claim 1, in combination with a physiologically acceptable carrier.

63. A pharmaceutical composition for the treatment if *Chlamydia* infection in a patient, comprising antigen presenting cells incubated in the presence of a polynucleotide of claim 3, in combination with a physiologically acceptable carrier.

64. A polypeptide comprising an immunogenic portion of a *Chlamydia* antigen, wherein said immunogenic portion comprises a sequence of SEQ ID NO: 18, 19, 31, 39, 93-96, 98, 100-102, 106, 108, 138-140, 158, 167, 168, 246, 247 and 254-256.

65. An immunogenic epitope of a *Chlamydia* antigen, comprising a sequence of SEQ ID NO: 31, 98, 106, 108, 138-140, 158, 167, 168, 246, 247 or 254-256.

66. An isolated polypeptide comprising a sequence recited in any one of SEQ ID NO: 5-14, 17-20, 26, 28, 30-32, 34, 39-43, 65, 89-109, 138-158, 167, 168, 224-262, 246, 247, 254-256 and 292.

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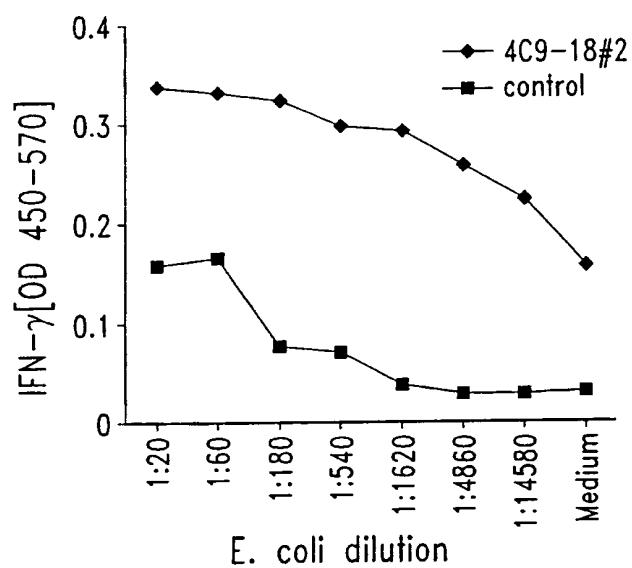
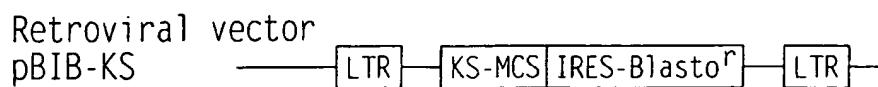


Fig. 1

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Kozak-Start

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A CGG CGG TGG TAC CTT AAG CTA TAG CCT AGG GAC GTC  
(BgIII) EcoRI BamHI PstI

AAG CTT GAG CTC GAG CGC GGC CGC TAA TTA GCT GAG      ReadingFrame 1  
TTC GAA CTC GAG CTC GCG CCG GCG ATT AAT CGA CTC AGC T  
HinDIII XhoI NotI Stop Stop Stop (SalI) KS1+

Kozak-Start

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A CGG CGG TGG TAC CCT TAA GCT ATA GCC TAG GGA CGT C  
(BgIII) EcoRI BamHI PstI

AA GCT TGA GCT CGA GCG CGG CCG CTA ATT AGC TGA G      ReadingFrame 1  
TT CGA ACT CGA GCT CGC GCC GGC GAT TAA TCG ACT CAG CT  
HinDIII XhoI NotI Stop Stop Stop (SalI) KS2+

Kozak-Start

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A CGG CGG TGG TAC CCC TTA AGC TAT AGC CTA GGG ACG TC  
(BgIII) EcoRI BamHI PstI

A AGC TTG AGC TCG AGC GCG GCC GGT AAT TAG CTG AG      ReadingFrame 3  
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HinDIII XhoI NotI Stop Stop Stop (SalI) KS3+

Fig. 2

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## Chlamydia C17.8 Peptide Screen

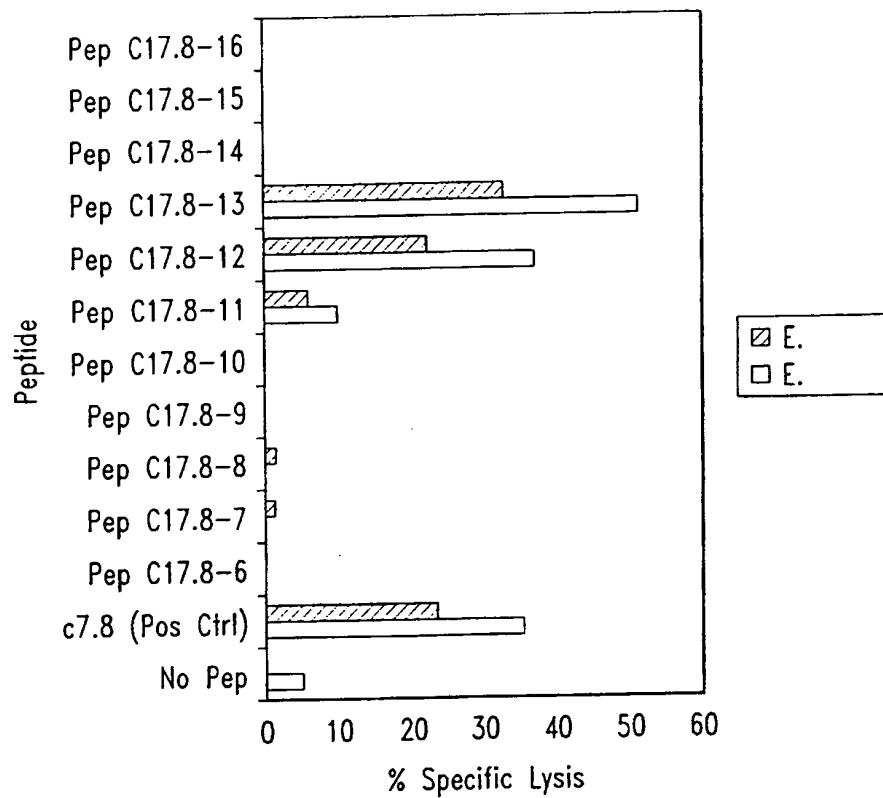
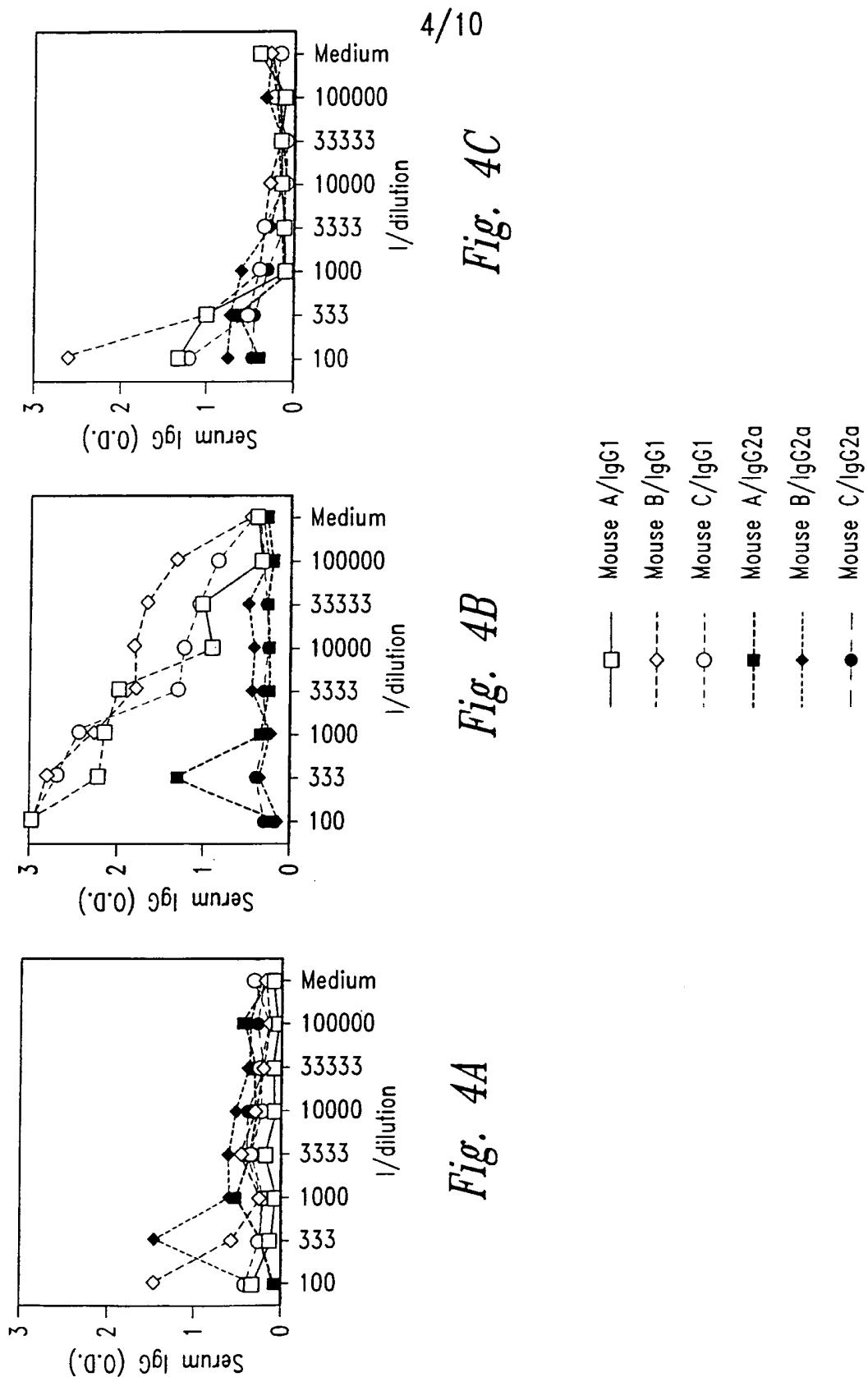
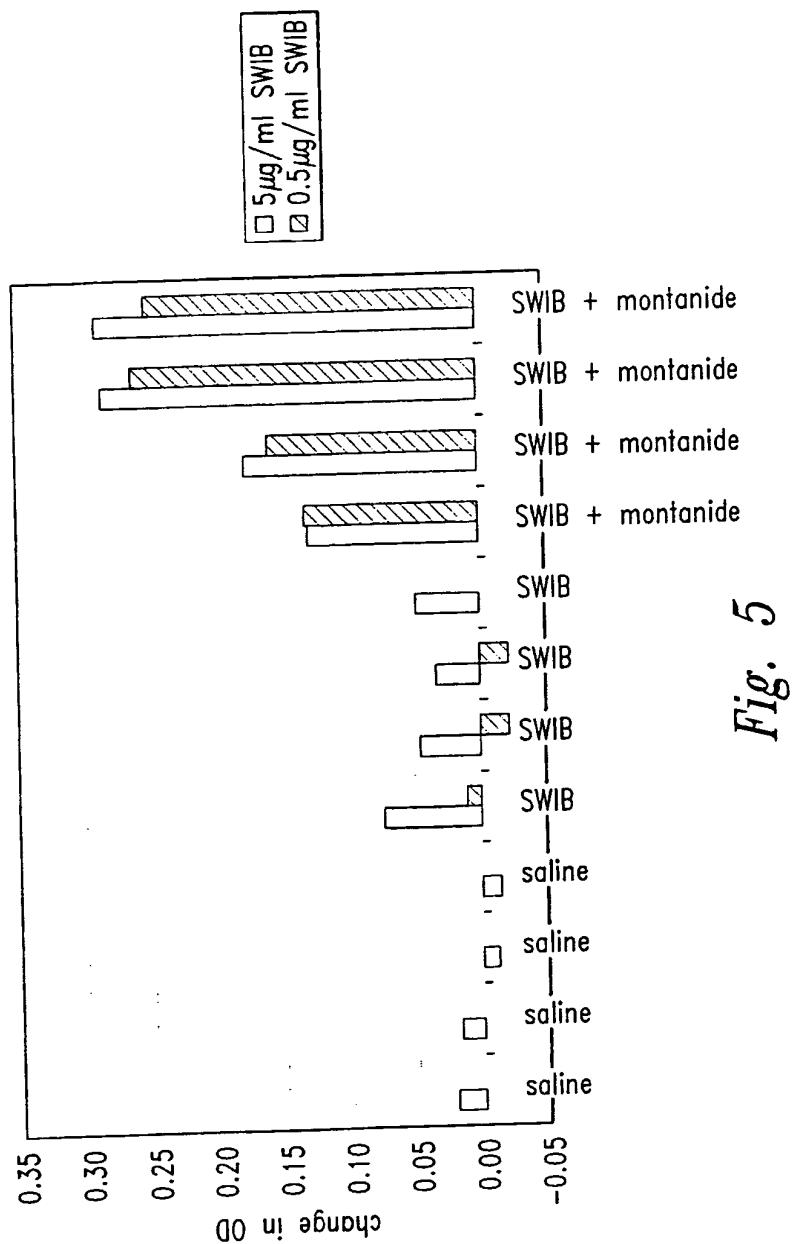


Fig. 3



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CP SWIB Nde (5' primer)

5' GATATACATATGCATCACCATCACCATCACATGAGTCAAAAAAATAAAAACCTCT

CP SWIB EcoRI (3' primer)

5' CTCGAGGAATTCTTATTTACAATATGTTGGA

CP S13 Nde (5' primer)

5' GATATACATATGCATCACCATCACCATCACATGCCACGCATCATTGGAATGAT

CP S13 EcoRI (3' primer)

5' CTCGAGGAATTCTTATTTCTTACCTGC

*Fig. 6*

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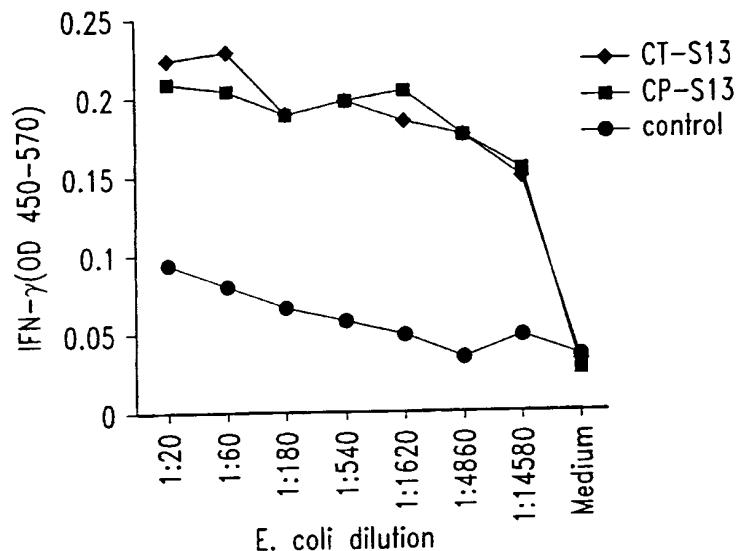


Fig. 7A

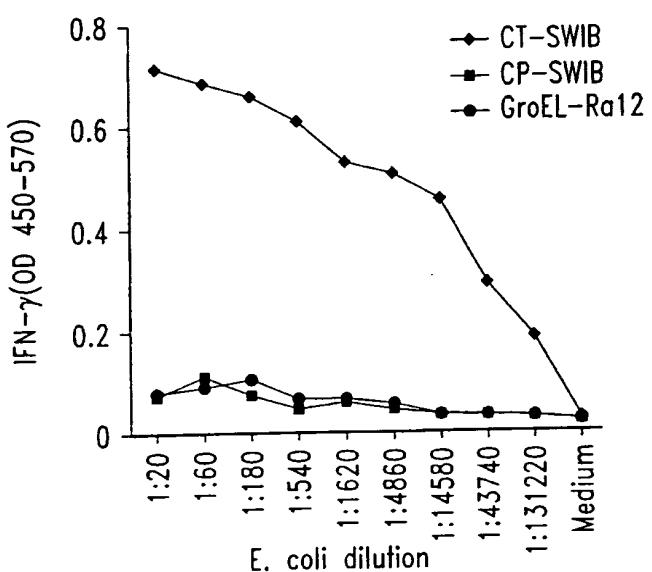


Fig. 7B

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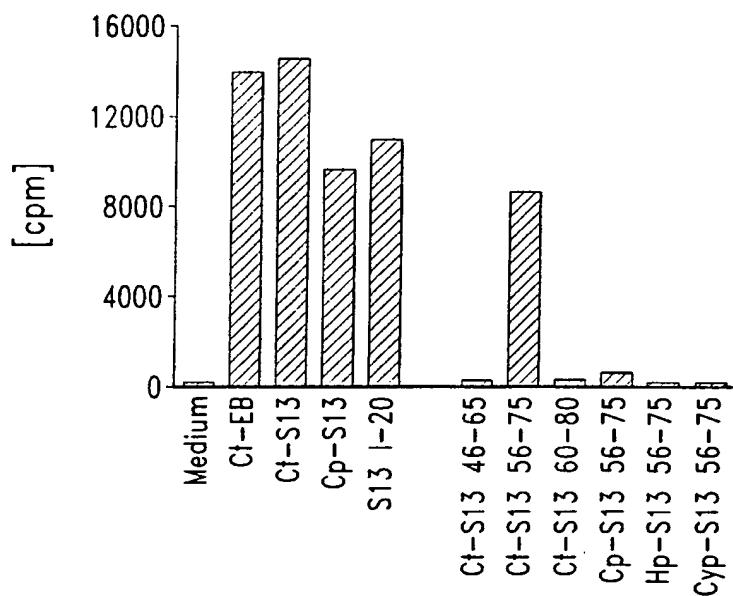


Fig. 8

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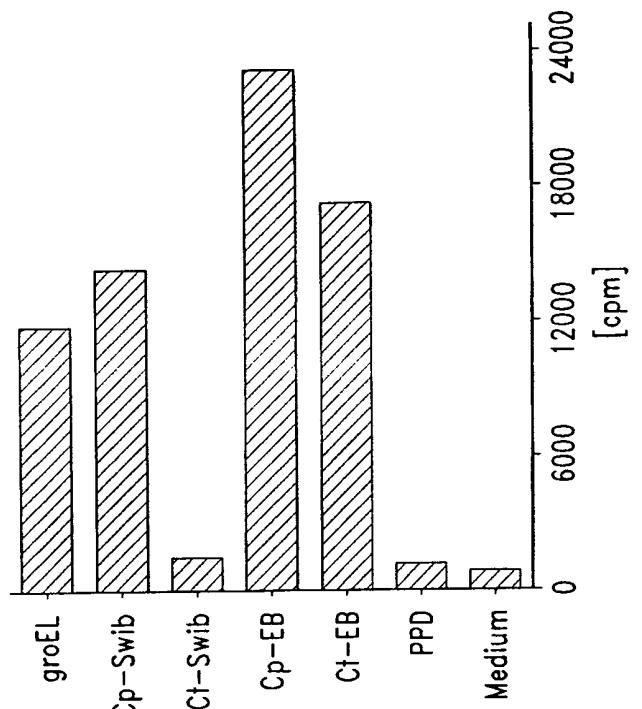


Fig. 9B

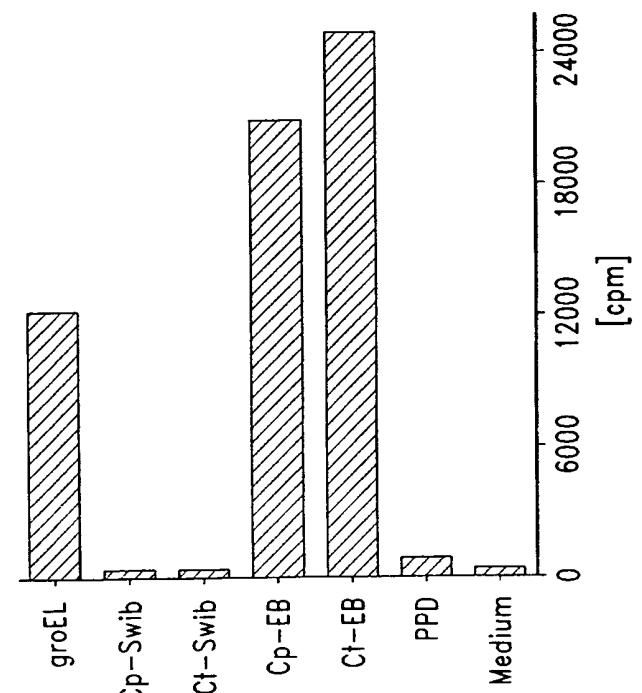


Fig. 9A

10/10

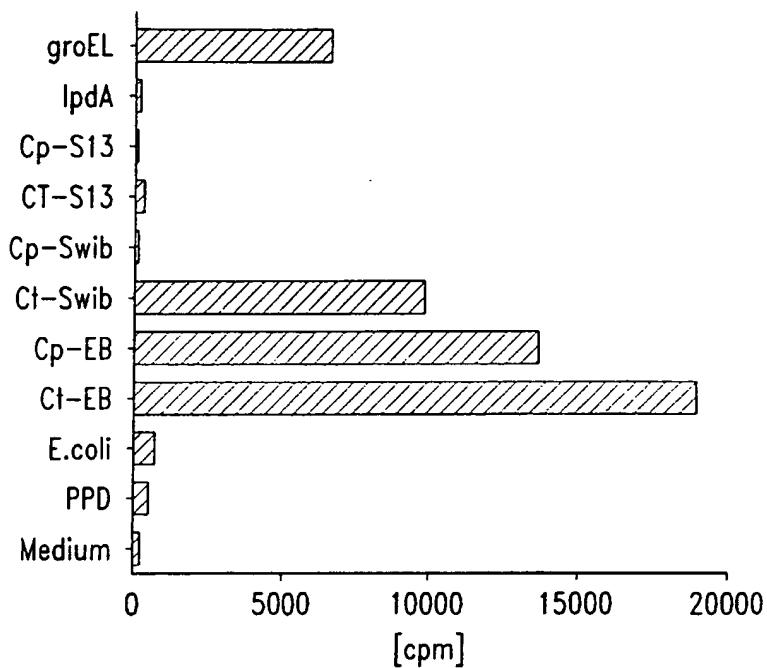


Fig. 10

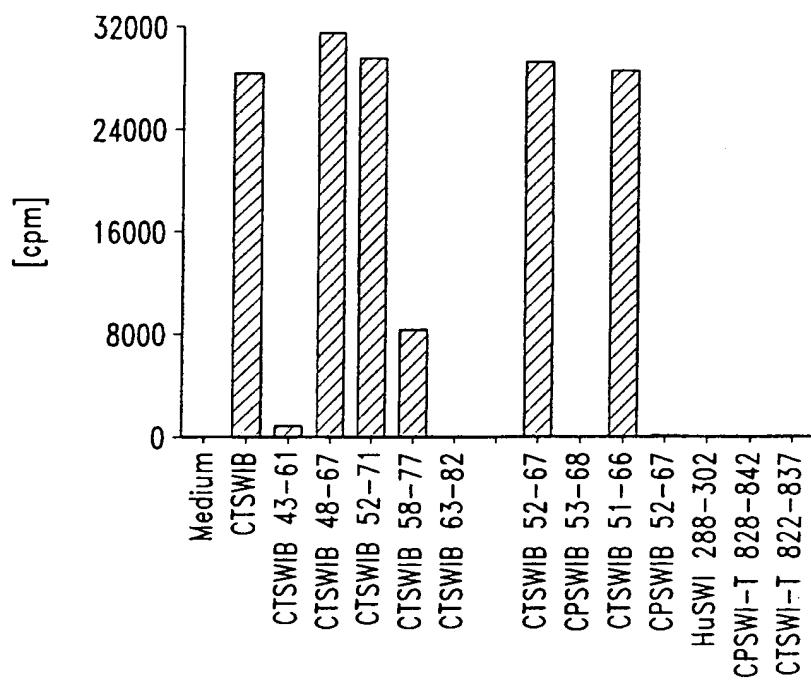


Fig. 11

## SEQUENCE LISTING

<110> Corixa Corporation  
Probst, Peter  
Bhatia, Ajay  
Skeiky, Yasir  
Fling, Steve  
Maisonneuve, Jeff

<120> COMPOSITIONS AND METHODS FOR TREATMENT AND  
DIAGNOSIS OF CHLAMYDIAL INFECTION

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<140> PCT  
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tagggccagc tttttctaaa gagattatttgc ttagattgcg tttttacag tcggattacg	180
ctgcagagtt gactgaggaa gaggttggtc gactaaacgc tctttacag tcggattacg	240
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caaattctcg cacgcgttaag ggttaaacgtaaactattgc aggttaagaag aaataataat	420
ttttaggaga gagtgttttg gttaaaaatc aagcgcaaaaa aagaggcgtaaagaaaac	480
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 <213> Chlamydia trachomatis

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Ile Ile Lys Met Trp Asp Tyr Ile Lys Glu Asn Ser Leu Gln Asp	
35 40 45	
Pro Thr Asn Lys Arg Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val	
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Phe Gly Thr Glu Lys Pro Ile Asp Met Phe Gln Met Thr Lys Met Val	
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Ser Gln His Ile Ile Lys	
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 <211> 61  
 <212> PRT  
 <213> Chlamydia trachomatis

<400> 6	
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Asn Ile Asn Pro Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys	
35 40 45	
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<211> 36  
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<213> Chlamydia trachomatis

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Gln Ser His Arg  
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<210> 8  
<211> 18  
<212> PRT  
<213> Chlamydia trachomatis

<400> 8  
Leu Arg His His Ala Ser Leu Gln Thr Asn Met Asp Ile Ser Asn Phe  
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Pro Phe

<210> 9  
<211> 5  
<212> PRT  
<213> Chlamydia trachomatis

<400> 9  
Leu Ala Leu Trp Asn  
1 5

<210> 10  
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<212> PRT  
<213> Chlamydia trachomatis

<400> 10  
Cys Cys Tyr Arg Val Asn His Asn His Ile Asp  
1 5 10

<210> 11  
<211> 36  
<212> PRT  
<213> Chlamydia trachomatis

<400> 11  
Val Asp Val Ile Val Ile Asp Ser Val Ala Ala Leu Val Pro Lys Ser  
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Glu Leu Glu Gly Glu Ile Gly Asp Val His Val Gly Leu Gln Ala Arg  
20 25 30  
Met Met Ser Gln  
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<210> 12

<211> 122  
<212> PRT  
<213> Chlamydia trachomatis

<400> 12  
Met Pro Arg Ile Ile Gly Ile Asp Ile Pro Ala Lys Lys Lys Leu Lys  
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Ile Ile Ala Arg Leu Gln Leu Asn Pro Glu Ala Arg Ala Ala Glu Leu  
35 40 45  
Thr Glu Glu Glu Val Gly Arg Leu Asn Ala Leu Leu Gln Ser Asp Tyr  
50 55 60  
Val Val Glu Gly Asp Leu Arg Arg Val Gln Ser Asp Ile Lys Arg  
65 70 75 80  
Leu Ile Thr Ile His Ala Tyr Arg Gly Gln Arg His Arg Leu Ser Leu  
85 90 95  
Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly  
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Lys Arg Lys Thr Ile Ala Gly Lys Lys Lys  
115 120

<210> 13  
<211> 20  
<212> PRT  
<213> Chlamydia trachomatis

<400> 13  
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Val Phe Gly Thr  
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<210> 14  
<211> 20  
<212> PRT  
<213> Chlamydia trachomatis

<400> 14  
Asp Asp Lys Leu Ala Lys Val Phe Gly Thr Glu Lys Pro Ile Asp Met  
1 5 10 15  
Phe Gln Met Thr  
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<210> 15  
<211> 161  
<212> DNA  
<213> Chlymidia trachomatis

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ttacctaccc cgcgacattc ggagctatcc gtcggattct gtttgtaac aaaatgctgg 120  
cgcaaccgtt tctttcttcc caaactaaag caaatatggg a 161

<210> 16

<211> 897  
<212> DNA  
<213> Chlymidia trachomatis

<400> 16

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attaagggtt ccaagtctgc	tgcgcattt accgcataa	tttggaca agctggaggc	180
gcgggcttt ccgcacacat	tacagttcc caagtgtcca	aaggattagg ggatgcgaga	240
actgttgtcg cttagggaa	tgccttaac ggagcgttgc	caggaacagt tcaaagtgcg	300
caaagcttc tctctcacat	gaaagctgtc agtcagaaaa	cgcaagaagg ggatgagggg	360
ctcacagcag atcttgcgt	gtctcataag cgcagagcgg	ctgcggctgt ctgtagcatc	420
atcgaggaa ttacctacct	cgcgcacattc ggagctatcc	gtccgattct gtttgtcaac	480
aaaatgctgg caaaaccgtt	tctttcttcc caaactaaag	caaataatggg atcttctgtt	540
agctatatta tggcggctaa	ccatgcagcg tctgtgggg	gtgctggact cgctatcagt	600
gcggaaagag cagattgcga	agccccgtgc gtcgtattt	cgagagaaga gtcgttactc	660
gaagtgcgg gagagggaaa	tgcttgcag aagaaagtgc	ctggagagaa accaagacg	720
ttcacgcga tcaagtatgc	actcctact atgctcgaga	agtttttggg atgcgttgcc	780
gacgtttca aatttggtgcc	gctgcctatt acaatggta	ttcgtgcgat tggctgtct	840
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<210> 17  
<211> 298  
<212> PRT  
<213> Chlamydia trachomatis

<400> 17

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Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala			
35	40	45	
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser			
50	55	60	
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg			
65	70	75	80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr			
85	90	95	
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln			
100	105	110	
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser			
115	120	125	
His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile			
130	135	140	
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn			
145	150	155	160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met			
165	170	175	
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val			
180	185	190	
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala			
195	200	205	
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly			
210	215	220	

Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr  
 225 230 235 240  
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu  
 245 250 255  
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met  
 260 265 270  
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 275 280 285  
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 <212> PRT  
 <213> Chlamydia trachomatis

<400> 18  
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 Tyr Leu

<210> 19  
 <211> 18  
 <212> PRT  
 <213> Chlamydia trachomatis

<400> 19  
 Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile  
 1 5 10 15  
 Arg Pro

<210> 20  
 <211> 216  
 <212> PRT  
 <213> Chlamydia trachomatis

<400> 20  
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 Ser Glu Leu Ser Val Arg Phe Cys Leu Ser Thr Lys Cys Trp Gln Asn  
 35 40 45  
 Arg Phe Phe Leu Pro Lys Leu Lys Gln Ile Trp Asp Leu Leu Ala  
 50 55 60  
 Ile Leu Trp Arg Leu Thr Met Gln Arg Leu Trp Trp Val Leu Asp Ser  
 65 70 75 80  
 Leu Ser Val Arg Lys Glu Gln Ile Ala Lys Pro Ala Ala Leu Val Leu  
 85 90 95  
 Arg Glu Lys Ser Arg Tyr Ser Lys Cys Arg Glu Arg Lys Met Leu Ala  
 100 105 110  
 Arg Arg Lys Ser Leu Glu Arg Lys Pro Arg Arg Ser Arg Ala Ser Ser  
 115 120 125

Met His Ser Ser Leu Cys Ser Arg Ser Phe Trp Asn Ala Leu Pro Thr  
 130 135 140  
 Phe Ser Asn Trp Cys Arg Cys Leu Leu Gln Trp Val Phe Val Arg Leu  
 145 150 155 160  
 Trp Leu Leu Asp Val Arg Ser Leu Leu Gln Leu Leu Asp Cys Ala Leu  
 165 170 175  
 Ser Ala Pro Glu His Lys Gly Phe Phe Lys Phe Leu Lys Lys Lys Ala  
 180 185 190  
 Val Ser Lys Lys Gln Pro Phe Leu Ser Thr Lys Cys Leu Ala Phe  
 195 200 205  
 Leu Ile Val Lys Ile Val Phe Leu  
 210 215

&lt;210&gt; 21

&lt;211&gt; 1256

&lt;212&gt; DNA

&lt;213&gt; Chlamydia trachomatis

&lt;400&gt; 21

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tcgggtgcga	attcgcttcc	ttatccata	cgtaggctc	cgaagtttct	gtgatcgaag	120
caagctctca	aatccttgct	ttgataatac	cagatatttc	aaaaccatg	tgcataaat	180
tcacccgaca	aggactccgt	ttcgtaactag	aagcctctgt	atcaaataatt	gaggatataag	240
gagatcgcgt	tcggtaact	atcaatggga	atgtcgaaga	atacgattac	gttctcgat	300
ctataggacg	ccgttgaat	acagaaaata	ttggcttggg	taaagctgg	gttattttgtg	360
atgaacgcgg	agtcatccct	accgatgcca	caatgcgcac	aaacgtacct	aacatttatg	420
ctattggaga	tatcacagga	aaatggcaac	ttgccccatgt	agtttctcat	caaggaatca	480
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tgattctttg	cgagaatttat	ccgcttaagct	tggttacgat	agcgatggag	agactggggaa	780
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tctagaatac	ccaagtgtcc	tccaggtgt	aataactcgat	acactccct	aagagcctct	1200
aatggatagg	ataagtcccg	taatccatag	gccatagaag	ctaaacgaaa	cgtatt	1256

&lt;210&gt; 22

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Chlamydia trachomatis

&lt;400&gt; 22

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tcgggtgcga	attcgcttcc	ttatccata	cgtaggctc	cgaagtttct	gtgatcgaag	120
caagctctca	aatccttgct	ttgataatac	cagatatttc	aaaaccatg	tgcataaat	180
tcacccgaca	aggactccgt	ttcgtaactag	aagcctctgt	atcaaataatt	gaggatataag	240
gagatcgcgt	tcggtaact	atcaatggga	atgtcgaaga	atacgattac	gttctcgat	300
ctataggacg	ccgttgaat	acagaaaata	ttggcttggg	taaagctgg	gttattttgtg	360
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ctattggaga	tatcacagga	aaatggcaac	ttgccccatgt	agtttctcat	caaggaatca	480

ttgcagcacg	aatataagg	ggccataaaag	aggaaatcg	ttactctgt	gtcccttctg	540
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a						601
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<212>	DNA					
<213>	Chlamydia trachomatis					
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tttgattctt	tgcgagaatt	atccgctaag	tttggttacg	atagcgatgg	agagactggg	180
gatttcttca	acgaggaga	cgacgacgaa	gaagaggaaa	tcaaaccgaa	gaaaactacg	240
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<210>	24					
<211>	363					
<212>	DNA					
<213>	Chlamydia trachomatis					
<400>	24					
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actttcttc	agatacgaat	aagcatagct	gttcccagaa	taaaaacggc	cgacgctagg	180
aacaacaaga	tttagataga	gcttgtgt	caggtaaact	gggttatatg	ttgctggcq	240
tgttagttct	agaataccca	agtgtccccc	aggttgaat	actcgatata	cttcctctaag	300
agcctcta	ggataggata	agttccgtaa	tccataggcc	atagaagcta	aacgaaacgt	360
att						363
<210>	25					
<211>	696					
<212>	DNA					
<213>	Chlamydia trachomatis					
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gcaagctctc	aaatccttgc	tttgcataat	ccagatattt	caaaaaccat	gttcgataaaa	180
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tctataggac	gccgttggaa	tacagaaaat	attggcttg	ataaagctgg	tgttattttgt	360
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catcccttc	ttcgttact	ttttctgaaa	aatttgatac	agaagaagaa	ttcctcgcac	660
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<210>	26					
<211>	231					
<212>	PRT					
<213>	Chlamydia trachomatis					
<400>	26					

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 20 25 30  
 Gly Ser Glu Val Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu  
 35 40 45  
 Asn Asn Pro Asp Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln  
 50 55 60  
 Gly Leu Arg Phe Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile  
 65 70 75 80  
 Gly Asp Arg Val Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp  
 85 90 95  
 Tyr Val Leu Val Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly  
 100 105 110  
 Leu Asp Lys Ala Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr  
 115 120 125  
 Asp Ala Thr Met Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp  
 130 135 140  
 Ile Thr Gly Lys Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile  
 145 150 155 160  
 Ile Ala Ala Arg Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser  
 165 170 175  
 Ala Val Pro Ser Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly  
 180 185 190  
 Leu Ser Pro Thr Ala Ala Gln Gln His Leu Leu Leu Arg Leu Leu Phe  
 195 200 205  
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 210 215 220  
 Glu Gly Val Trp Lys Thr Ser  
 225 230

<210> 27  
 <211> 264  
 <212> DNA  
 <213> Chlamydia pneumoniae

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 tacattaaaa aacacaactg tcaggatcaa aaaaataaac gtaatatcct tcccgatgcg 180  
 aatcttgcca aagtcttgg ctctagtgtat cctatcgaca tgttccaaat gaccaaagcc 240  
 ctttccaaac atattgtaaa ataa 264

<210> 28  
 <211> 87  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 28  
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 1 5 10 15  
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 20 25 30  
 Glu Ile Val Lys Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln  
 35 40 45

Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys  
 50 55 60  
 Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala  
 65 70 75 80  
 Leu Ser Lys His Ile Val Lys  
 85

<210> 29  
 <211> 369  
 <212> DNA  
 <213> Chlamydia pneumoniae

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 cctgaggcaa gagccctctga attaactgaa gaagaagtag gacgactgaa ctctctgcta 180  
 caatcagaat ataccgtaga aggggatttg cgacgtcggt ttcaatcgga tatcaaaaaga 240  
 ttgatcgcca tccatttctta tcgaggtcag agacatagac tttctttacc agtaagagga 300  
 caacgtacaa aaactaattc tcgtactcga aaaggtaaaa gaaaaacagt cgccaggtaag 360  
 aagaaaataa 369

<210> 30  
 <211> 122  
 <212> PRT  
 <213> Chlamydia pneumoniae

<400> 30  
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 20 25 30  
 Ile Ile Lys Leu Lys Leu Asp Pro Glu Ala Arg Ala Ser Glu Leu  
 35 40 45  
 Thr Glu Glu Glu Val Gly Arg Leu Asn Ser Leu Leu Gln Ser Glu Tyr  
 50 55 60  
 Thr Val Glu Gly Asp Leu Arg Arg Arg Val Gln Ser Asp Ile Lys Arg  
 65 70 75 80  
 Leu Ile Ala Ile His Ser Tyr Arg Gly Gln Arg His Arg Leu Ser Leu  
 85 90 95  
 Pro Val Arg Gly Gln Arg Thr Lys Thr Asn Ser Arg Thr Arg Lys Gly  
 100 105 110  
 Lys Arg Lys Thr Val Ala Gly Lys Lys Lys  
 115 120

<210> 31  
 <211> 10  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Made in the lab

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 1 5 10

<210> 32  
<211> 53  
<212> PRT  
<213> Chlamydia trachomatis

<400> 32  
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35 40 45  
Lys Ala Asn Met Gly  
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<210> 33  
<211> 161  
<212> DNA  
<213> Chlamydia trachomatis

<400> 33  
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caaaaaccgtt tctttttcc caaactaaag caaatatggg a 161

<210> 34  
<211> 53  
<212> PRT  
<213> Chlamydia trachomatis

<400> 34  
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35 40 45  
Lys Ala Asn Met Gly  
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<210> 35  
<211> 55  
<212> DNA  
<213> Chlamydia pneumoniae

<400> 35  
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<210> 36  
<211> 33  
<212> DNA  
<213> Chlamydia pneumoniae

<400> 36

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<211> 53  
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<213> Chlamydia pneumoniae  
  
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<210> 38  
<211> 30  
<212> DNA  
<213> Chlamydia pneumoniae  
  
<400> 38  
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<210> 39  
<211> 16  
<212> PRT  
<213> Artificial Sequence  
  
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<223> Made in the lab  
  
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<213> Artificial Sequence  
  
<220>  
<223> made in the lab  
  
<400> 40  
Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser  
1 5 10 15  
  
<210> 41  
<211> 15  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> made in the lab  
  
<400> 41  
Lys Glu Tyr Ile Asn Gly Asp Lys Tyr Phe Gln Gln Ile Phe Asp  
1 5 10 15

<210> 42  
<211> 16  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> made in the lab

<400> 42  
Lys Lys Ile Ile Ile Pro Asp Ser Lys Leu Gln Gly Val Ile Gly Ala  
1 5 10 15

<210> 43  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> made in the lab

<400> 43  
Lys Lys Leu Leu Val Pro Asp Asn Asn Leu Ala Thr Ile Ile Gly  
1 5 10 15

<210> 44  
<211> 509  
<212> DNA  
<213> Chlamydia

<400> 44  
ggagctcgaa ttccggcacga gagtcctat tgtttgcag gctttgtctg atgatagcga 60  
taccgtacgt gagattgcgt tacaagtgcg tggttatgtat gggttctagtt gcttaactgcg 120  
cgccgtgggc gatttagcga aaaatgatcc ttcttattcaa gtacgcata ctgcttatcg 180  
tgctgcagcc gtgttggaga tacaagatct tgtgcctcat ttacgagttg tagtccaaaa 240  
tacacaatta gatggAACGG aaagaagaga agcttggaga tctttatgtg ttcttactcg 300  
gcctcatagt ggtgtattaa ctggcataga tcaagctta atgaccgttg agatgtaaa 360  
ggaatatcct gaaaagtgtt cggaaaca gattcgatca ttattggctg cagatcatcc 420  
agaagtgcag gtagctactt tacagatcat tctgagagga ggttagagtat tccggcatac 480  
ttctataatg gaatcggttc tcgtgccgg 509

<210> 45  
<211> 481  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (23)  
<223> n=A,T,C or G

<400> 45  
gatccgaatt cggcacgagg cantattac tcccaacatt acggttccaa ataagcgata 60  
aggcttcta ataaggaagt taatgtaaaga ggcttttta ttgctttcg taaggttagta 120  
ttgcaaccgc acgcgattga atgatacgca agccattcc atcatggaaa agaacccttg 180  
gacaaaaata caaaggaggt tcactcctaa ccagaaaaag ggagagttttag tttccatggg 240

ttttccttat atacacccgt ttcacacaat taggagccgc gtctagtatt tggaatacaa 300  
attgtccccca agcgaatttt gttcctgtt cagggatttc tcctaattgt tctgtcagcc 360  
atccgcctat ggtAACGCAA ttagctgttag taggaagatc aactccaaac aggtcataga 420  
aatcagaaaag ctcataggtg cctgcagcaa taacaacatt cttgtctgag tgagcgaatt 480  
g 481

<210> 46  
<211> 427  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (20)  
<223> n=A,T,C or G

<400> 46

gatccgaatt cgqcacgagn ttttcctgt ttttccttag ttttagtgt tccccggagca 60  
ataacacaga tcaaagaacg gccattcagt ttaggctctg actcaacaaa acctatgtcc 120  
tctaaagccct gacacattct ttgaacaacc ttatgcccgt gttcgggata agccaactct 180  
cgcccccgaa acatacaaga aacctttact ttatccctt tctcaataaaa ggctctagct 240  
tgcttgctt tcgtaagaaaa gtcgttatca tcgatattag gcttaagctt aacctcttg 300  
atacgcactt ggtgctgtgc ttcttacta tcttttctt ttttagttat gtcgtaacga 360  
tacttccgt agtccatgat ttgcacaca ggaggctctg agttgaagc aacctcgatc 420  
cgaattc 427

<210> 47  
<211> 600  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (522)  
<223> n=A,T,C or G

<400> 47

gatccgaatt cgqcacgaga tgcttctatt acaattgggtt tggatgcgga aaaagcttac 60  
cagcttattc tagaaaagtt gggagatcaa attcttgggtt gaattgctga tactattgtt 120  
gatagtagacag tccaagatat tttagacaaa atcacaacag acccttctct aggtttgtt 180  
aaagctttt acaactttcc aatcactaat aaaattcaat gcaacgggtt attcaactccc 240  
aggaacattt agaacttttattt aggaggaact gaaataggaa aattcacagt cacacccaaa 300  
agctctggga gcatgttctt agtctcagca gatattattt catcaagaat ggaaggcggc 360  
gttggcttag ctgtggtagt agaaggttat gtcgtaccc acgcgtttagt ttatggatac 420  
tcatcaggcg ttccctaattt atgttagtcta agaaccagaa ttattaatac aggattgact 480  
ccgacaacgt attcattacg tggatggcggt ttagaaagcg gngtggatg ggttaatgcc 540  
ctttctaattg gcaatgatattt tttaggaata acaaatttcc taatgtatct ttttggagg 600

<210> 48  
<211> 600  
<212> DNA  
<213> Chlamydia

<400> 48

ggagctcgaa ttccggcacga gctctatgaa tatccaattt tctaaactgt tcggataaaaa 60

atgatgcagg aattaggtcc acactatctt tttttgttc gcaaatgatt gattttaaat 120  
cgtttgatgt gtatactatg tcgtgtaaagc cttttgggtt acttctgaca ctagccccca 180  
atccagaaga taaaattggat tgcggttcta ggtcagcaag taacactttt ttccctaaaa 240  
attgggccaa gttgcattccc acgttttagag aaagtgttgtt ttttccagtt cttcccttaa 300  
aagagcaaaa aactaagggtg tgcaaatcaa ctccaaacgtt agagtaagtt atctattcag 360  
ccttggaaaa catgtctttt ctagacaaga taagcataat caaagccttt ttagcttta 420  
aactgttatac ctctaaattt tcaagaacag gagagtctgg gaataatcct aaagagtttt 480  
ctatttgttg aagcagtctt agaatttagtgc agacactttt atggtagagt tctaagggg 540  
aatttaagaa agttactttt tccttgcattt ctcgtatttt taggtctaat tcggggaaa 600

<210> 49  
<211> 600  
<212> DNA  
<213> Chlamydia

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<400> 49
gatccgaatt cggcacgaga tgcttctatt acaattgggtt tggatgcggaa aaaagcttac 60
cagcttattc tagaaaagtt gggagatcaa attcttggtt gaattgtcgaa tactattgtt 120
gatagtacag tccaaagatata tttagacaaa atcacaacag accccttcctt aggttttgtt 180
aaagctttta acaactttcc aatcactaat aaaattcaat gcaacgggtt attcaactccc 240
aggaacattt gaaattttattt aggaggaact gaaataggaa aattcacagt cacacccaaa 300
agctctggaa gcatgttctt agtctcagca gatattattt catcaagaat ggaaggcggc 360
gttggtagt ctttggtagc agaagggttatc tctaaggccct acgcgcattttt ttatggat 420
tcatcaggcg ttccaaattt atgt.agtcta agaaccagaa ttatataatc aggattgtact 480
ccgacaaacgt attcattacg tgtaggcgtt ttagaaagcg gtgtggatgt ggtaatgcc 540
ctttctaata gcaatgtat ttttaggaata acaaataactt ctaatgtatc ttttttgag 600

```

<210> 50  
<211> 406  
<212> DNA  
<213> Chlamydia

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<400> 50
gatccgaatt cgccacgggt tcttagcttg ctttaattacg taattaacca aactaaagg 60
gctatcaaat agcttattca gtctttcatt agttaaacga tcttttctag ccatgactca 120
tccttatgttc ttcaagctata aaaatacttc ttaaaacttg atatgcgtta atcaaatcat 180
cattaaccac aacataatca aattcgcgtag cgccagcaat ttgcacagcg ctatgccta 240
atctttcttt ctctggaaa tctttctctg aatcccgagc attcaaacgg cgctcaagt 300
cttcttgaga gggagcttga ataaaaatgt gactgccgac atttgcttct tcagagccaa 360
agcttccttgt acatcaatca cggtatgca gtctcggtcc gaattc 406

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<210> 51  
<211> 602  
<212> DNA  
<213> Chlamydia

gaggttaatac ctcaaacaaa cgcttaaaca attttattt gattttctt ataggttta 540  
tattagaga aaaaagttcg aattacgggg tttgttatgc aaaataaaact cgtgccaat 600  
tc 602

<210> 52  
<211> 145  
<212> DNA  
<213> Chlamydia

<400> 52  
gatccgaatt cggcacgagc tcgtgccat gtgtcaaca gcatccatag gatgggcagt 60  
caaataact ccaagtaatt cttttctct tttcaacaac tccttaggag agcgttggat 120  
aacatttca gtcgtgccg aattc 145

<210> 53  
<211> 450  
<212> DNA  
<213> Chlamydia

<400> 53  
gatccgaatt cggcacgagg taatcggcac cgcactgctg acactcatct cctcgagctc 60  
gatcaaaccc acacttggga caagtaccta caacataacg gtccgataaa aacttccctt 120  
cttcctcaga atacagctgt tcggtcacct gattctctac cagtcgcgt tcctgcaagt 180  
ttcgatagaa atcttgaca atagcaggat gataagcggt cgtagttctg gaaaagaaaat 240  
ctacagaaat tcccccaatttc ttgaaggat ctttatgaag cttatgatac atgtcgacat 300  
attcttgata ccccatgcct gccaactctg cattaagggt aattgcgatt ccgtattcat 360  
cagaaccaca aatatacaaa acctcttgc cttgtatgtct ctgaaaacgc gcataaacat 420  
ctgcaggcaa ataagcctcg tgccgaattc 450

<210> 54  
<211> 716  
<212> DNA  
<213> Chlamydia

<400> 54  
gatcgaaatt cggcacgagc ggcacgagtt ttctgatagc gatttacaat cctttattca 60  
actttgcct agagaggcac actataactaa gaagtttctt gggtgtgtgg cacagtccctg 120  
tcgtcagggg attctgctag aggggttaggg gaaaaaaccctt ttattactat gaccatgcgc 180  
atgtgaaatt acatccata gactttcgca tcattcccaa catttacaca gctctacacc 240  
tcttaagaag aggtgacgtg gattgggtgg ggcagccctg gcaccaaggg attccttttg 300  
agcttcggac tacctctgtc ctctacaccc attaccctgt agatggcaca ttctggctt 360  
ttcttaatcc caaagatcct gtacttcct ctctatctaa tcgtcagcga ttgattgctg 420  
ccatccaaaa ggaaaaactg gtgaagcaag ctttaggaac acaatatcga gtagctgaaa 480  
gctctccatc tccagaggga atcatagctc atcaagaagc ttctacttcct tttcctggga 540  
aaattacttt gatatatccc aataatatta cgcgtgtca gcgtttggcc gaggtatcca 600  
aaaaatgatc gacaaggagc acgctaaatt tgtacatacc caaaaatcaa tcagccatct 660  
aggcaatgg aatatcaaag taaacagttt acaactgggg atctcggtgcc gaattc 716

<210> 55  
<211> 463  
<212> DNA  
<213> Chlamydia trachomatis

<400> 55  
tctcaaatcc ttgctttgaa taatccagat atttcaaaaaa ccatgttcga taaattcacc 60

cgacaaggac tccgttgcgt actagaagcc tctgtatcaa atattgagga tataggagat 120  
 cgcgttcgggt taactatcaa tggaaatgtc gaagaatacg attacgttct cgtatctata 180  
 ggacgccgtt tgaatacaga aaatattggc ttggataaag ctgggtttat ttgtgtgaa 240  
 cgcggagtca tccctaccga tgccacaatg cgcacaaaacg tacctaacat ttatgttatt 300  
 ggagatatac cagaaaaatg gcaacttgcc catgttagctt ctcatcaagg aatcattgca 360  
 gcacggaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgatc 420  
 tttaccttcc ctgaagtcgc ttcatggc ctctccccaa cag 463

<210> 56  
 <211> 829  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 56  
 gtactatggg atcatttagtt ggaagacagg ctccggattt ttctggtaaa ggcgttgg 60  
 gtggagaaga gaaagaaaatc tctctagcg actttcgtgg taagtatgtt gtgtctttct 120  
 tttatcctaa agattttacc tatgtttgtc ctacagaatt acatgtttt caagatagat 180  
 tggtagattt tgaagagcat ggtcgttcg ttcttgggtt ctccgttgac gacattgaga 240  
 cacattctcg ttggctact gtagcggag atgcaggagg gatagaggaa acagaatatac 300  
 ctctgttagc agacccctct tttaaaatat cagaagctt tgggttttg aatcctgaaag 360  
 gatcgtcgc ttaaagagct actttctta tcgataaaca tggggtttatt cgtcatgccc 420  
 ttataaatga ttcttcctta gggcgttcca ttgacgagga attgcgtatt ttagattcat 480  
 ttagtctttt tgagaaccac ggaatggttt gtccagctaa ctggcgttct ggagagcgtg 540  
 gaatggtgcc ttctgaagag ggattaaaag aatacttcca gacgatggat taagcatctt 600  
 tgaaaatgtaa agatcgtac agatcttgc tcaataatgt tgaagtctcc gacaccaggc aatgctaagg 720  
 tgcagagagc cagcggaggt tcaataatgt tgaagtctcc gacaccaggc aatgctaagg 780  
 cgacgatatt agttatgtgaa gtctgagttt taaggaaatg aaggccaaag aaatagctat 829  
 caataaagaa gccttcttcc ttgactctaa agaatagtat gtcgtatcc

<210> 57  
 <211> 1537  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 57  
 acatcaagaa atagcggact cgccttagt gaaaaaaagct gaggagcaga ttaatcaagc 60  
 acaacaagat attcaaaca tcaacacctag tgggttggat attcctatcg ttggtccgag 120  
 tgggtcagct gttcccgca gaaatgcggc aggagcgttg aaatcctcta acaattcagg 180  
 aagaatttcc ttgttgcgt atgatgtaga caatgaaaatg gcagcgattt caatgcaagg 240  
 ttttcgatct atgatcgaac aatttaatgt aaacaatctt gcaacagcta aagagctaca 300  
 agctatggag gtcagctga ctgcgtgtc agatcaactg gttggtgcgg atggcgagct 360  
 cccagccgaa atacaagcaa tcaaaatgc tcttgcgca gctttgaaac aaccatcagc 420  
 agatggttt gtcacagctt tgggacaagt ggcttttgc gtcggccagg ttggaggagg 480  
 ctccgcagga acagctggca ctgtccagat gaatgtaaaaa cagctttaca agacagcgtt 540  
 ttcttcgact tcttccagct ttatgcgtc agactttcc gatggatatt ctgcttacaa 600  
 aacactgaac tctttatatt ccgaaagcag aagcggcggt cagtcagctt ttatgtcaaac 660  
 tgc当地atccc ggcgtttcca gaagcgtttc tcgttctggc atagaatgtc aaggacgcag 720  
 tgcagatgtc agccaaagag cagcggaaac tattgtcaga gatagccaaa cgttaggtga 780  
 tgttatatac cgttacagg ttctggattt ttgtatgtct acgattgtga gcaatccgca 840  
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 tgggtatcc tctgttcaga attctgtggc tagttgcgtt aagtttgcgtt cacaattggc 960  
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 acagccccgtt ttcatcaac aggtgttgcgtt aaacattgtc tctctattctt ctgggttatctt 1080  
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 ggctttttt tcttttcaaa ggaatctcggtt gtctacagaa gtcctttcaa taataagttc 1200

ttagttccaa aagaagaaaa tatataaaaag aaaaaactcc taattcattt aaaaagtgc 1260  
 cggcagactt cgtggaaaat gtctgtaaag ctggaggggg atcagcagaa agatgcaaga 1320  
 tatccgagaa aaaaggctca ggctcgcc gaattcggca cgagactacg aaagaaaggt 1380  
 cttttcttcc ggaatctgtc attggatctg cgtaaagactt aaagttcgcc aacacaggct 1440  
 ctgtcttc tttaggtttc ttgcgcgaga aaaattttct caagtaacaa gaagatttct 1500  
 ttttacagcc ggcatccggc ttctcgca gtataac 1537

<210> 58  
 <211> 463  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 58  
 tctcaaatcc ttgctttgaa taatccagat atttcaaaaa scatgttcga taaattcacc 60  
 cgacaaggac tccgtttcgt actagaagcc tctgtatcaa atattgagga tataggagat 120  
 cgcgttcgtt taactatcaa tggaaatgtc gaagaatacg attacgttct cgtatctata 180  
 ggacgccgtt tgaatacaga aaatattggc ttggataaag ctgggtttat ttgtatgaa 240  
 cgcggagtca tcctaccga tgccacaatg cgacacaaacg tacctaatacat ttatgttatt 300  
 ggagatatac caggaaaatg gcaacttgcc catgtagctt ctcatcaagg aatcatggca 360  
 gcacgaaata taggtggcca taaagaggaa atcgattact ctgctgtccc ttctgtgatc 420  
 tttacccccc ctgaagtcgc ttcatgttagc ctctccccaa cag 463

<210> 59  
 <211> 552  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 59  
 acattccccc tgctcctcgc ggccatccac aaattgaggt aacccatcgat attgtatgcca 60  
 acggaatttt acacgtttct gctaaagatg ctgtatgtgg acgcqaaacaa aaaatccgt 120  
 ttgaagcaag ctctggatta aaagaagatg aaattcaaca aatgtatccgc gatgcagagc 180  
 ttcataaaaga ggaagacaaa caacgaaaag aagttctgtc tggaaaaat gaagccgatg 240  
 gaatgtatctt tagagccgaa aaagctgtc aagattacca cgacaaaatt cctgcagaac 300  
 ttgttaaaga aattgaagag catattgaga aagttccca agcaatcaaa gaagatgctt 360  
 ccacaacagc tatcaaagca gcttctgtatg agttgatgtc tcgtatgaa aaaatccggag 420  
 aagctatgca ggctcaatcc gcatccgcag cagcatcttc tgcagcgaat gctcaaggag 480  
 ggccaaacat taactccgaa gatctgaaaa aacatagttt cagcacacga cctccagcag 540  
 gaggaagcgc ct 552

<210> 60  
 <211> 1180  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 60  
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 cttttaggag aaaaaatcta taatgtcaga aaaatccgtc gtaaggatca cttccctca 120  
 acaactttttt catcttggat agagtttagtt tttagaacta agtcttctgc ttacaatgct 180  
 cttgcataattt acggatctttt tataaaatccccc cccacccaaa ctctacaaaaa agagtttcaa 240  
 tcgatccccat ataaaatccgc atatatttg gcccgttagaa aaggcgatatt aaaaaccaag 300  
 gtcgatgtga tagggaaatgt atgtggatc tcgtgcccggaa ttccggcacgaa gcccgcacgag 360  
 gatgtatgtatgaaatgtatgtaa agagctgcattt aattatgaca aagcatgaa aacgcattcg 420  
 tggatccaa gagacttacg atttatgttca gtcgtatctt ttgggtgaaag cgatagat 480  
 tttaaaacag tgcctactg tgcgttccgaa tcaaacgggtt gatgtgtctg taaaatttagg 540  
 gatcgatcca agaaagagtg atcagcaaat tcgtggatcg gtttcttac ctcacggat 600

aggtaaagtt ttgcgaattt tagttttgc tgctggagat aaggctgcag aggctattga 660  
 agcaggagcg gactttgtt gtagcgaacg cttggtagaa aaaatcaaag gtggatgggt 720  
 tgacttcgat gttcggttg ccactcccgaa tatgtatgaga gaggtcgaa agctaggaaa 780  
 agtttaggt ccaagaaacc ttatgcctac gcctaaagcc ggaactgtaa caacagatgt 840  
 gttaaaact attgcggAAC tgcgaaaagg taaaattgaa tttaaagctg atcgagctgg 900  
 tgtatgcac gtcggagttt cgaagcttc tttcgatagt gcgaaatca aagaaaatgt 960  
 tgaagcgttt tgcggccct tagttaaagc taagccgcac actgctaaag gacaatattt 1020  
 agttaatttc actatccct cgaccatggg gcaggggtt accgtggata ctaggagtt 1080  
 gattgcgtt taattctaag tttaaagagg aaaaatgaaa gaagagaaaa agttgctgct 1140  
 tcgcgagggtt gaagaaaaga taaccgcttc tcggcacgag 1180

<210> 61  
<211> 1215  
<212> DNA  
<213> Chlamydia trachomatis

<400> 61  
 attacagcgt gtgcaggtaa cgacatcatt gcatgatgct tttgatggca ttgatgcggc 60  
 attccttata gggtcagttc ctagaggccc aggaatggag agaagagatc ttctaaagaa 120  
 aaatggggag attgttgcata cgcaaggaaa agctttgaac acaacagcca agcgggatgc 180  
 aaagattttt gttgttggga accctgtgaa taccaattgc tggatagcaa tgaatcatgc 240  
 tcccagattt ttgagaaaaga actttcatgc gatgtacgaa ttggaccaga atcgatgc 300  
 tagcatgtt tcgcatagag cagaagtacc tttatcggtt gatatcacaag ttgtggttt 360  
 gggaaatcac tccgc当地 acatgcctga ttttacgca gctctgatta atgaccgtcc 420  
 tatcgcagag acgatagcgg atcgttattt gtttagagaat attatgtgc ttctgtaca 480  
 gagtcgttgtt agtgcagtaa ttgaagcacg agggaaagtct tcggcagctt ctgcagcacg 540  
 agcttagca gaggctgttc gatcaatata tcagccaaaaa gaaggactcg tgccgaaattc 600  
 ggcacgatc tcgaaattgc aggcttttct agtgaatggt cgtatgccta taaactacgt 560  
 ggtacagact tgagctctca aaagtttgc acagattctt acatcgcaga cccttattct 720  
 aagaatatct actccccctca actatttggaa tcccctaaac aagaaaagga ttacgcattt 780  
 agttacctga aatatgagga ttttactgg gaaggcgaca ctctttgc cctccaaaaa 840  
 gaaaattact tcatttatga aatgcatgtt cggtcattca cccgagatcc gtcttccag 900  
 gttccctatc ctggaaactt ccttggatc atcgaaaaaa tagaccacct caaacaacta 960  
 ggcgttcatg cagttgaact ccttcttatt ttcgaattcg atgaaaccgt ccatccattt 1020  
 aaaaatcagg acttccccca cctgtgtaac tattgggggtt attctcggtt gaattttttc 1080  
 tgcccctctc gccgttatac ttatggggca gacccttgcg ctccggcccg agagttcaag 1140  
 acttctgtca aagcgttaca ccgtgcggga atcgaagtca ttctcgatgt cgttttcaat 1200  
 catacaggct ttgaa 1215

<210> 62  
<211> 688  
<212> DNA  
<213> Chlamydia trachomatis

<400> 62  
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 ctaaacatctt atcagcgtca tctttgagaa gcatctaat gagcgtttt tcttctctag 120  
 catgccgcac atccgcttct tcattttctg taaaatatgc atagcttca ggattggaaa 180  
 atccaaagta ctcaat ccacgaaattt tctctctagc gatacgtgaa atttgcattt 240  
 catabaaata caaaggcagcc actcctgcag ctaaagaatc tcctgtacac caccgcattga 300  
 aagtagctac tttcgctttt gctgttccat taggctcatg agcctctaaac tcttctggag 360  
 taactccat agcaaaacaca aactgcttcc acaaataat atgatttaggg taaccgttct 420  
 ctcatccat caagttatct aacaataact tacgcgcctc taaaatcatcg caacgactat 480  
 gaatcgcaga taaaatatttta ggaaaggctt tgatatgtaa ataatagtct ttggcacgag 540  
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<210> 63  
 <211> 269  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 63  
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 gtgaagcaga gttcgtacgc agtgtatccag cgacaactcc tactgtgtat ggtaagctag 180  
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<210> 64  
 <211> 1339  
 <212> DNA  
 <213> Chlamydia trachomatis

<400> 64  
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 agcttagttaa tccttaggaa acatttctgg acctatgccc atcacattgg ctccgtatc 240  
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 caccattctc tcaataaaatc caatagcttt tcctgcacgg ctatgtatc gcccgtccg 420  
 gatagtattc actcggactc cccaaacgtcg gccggcttcc caagccagta ctttgcgt 480  
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 tggaaaaacag gttttat 1339

<210> 65  
 <211> 195  
 <212> PRT  
 <213> Chlamydia trachomatis

<400> 65  
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Val Val Cys Gly Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg Gly

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Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu Glu		
50	55	60
His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr His		
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Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly Thr		
85	90	95
Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe		
100	105	110
Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu		
115	120	125
Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro		
130	135	140
Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu Ile		
145	150	155
Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser Gly		
165	170	175
Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe Gln		
180	185	190
Thr Met Asp		
195		

<210> 66  
 <211> 520  
 <212> DNA  
 <213> Chlamydia

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 gatgaaggag atgtatttgc tctgaaagca aaggttctg aagctaacag aacattgcgt 240  
 cctccaacaa tcgcctgagg attctggctc atcagttgat gctttgcctg aatgagagcg 300  
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 tcatcgaacg aatttttcaa tcctcgaaaa tcttctccag agacttcgga aagatcttct 480  
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<210> 67  
 <211> 276  
 <212> DNA

<213> Chlamydia

<400> 67

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caagggcact atcaggaccc aagagctca gattatgacc tcccacgtgc tagcgactat 180  
gatttgccct aagccccata tcctactcca cctttgcctt ctagatatca gctacagaat 240  
atggatgttag aagcagggtt ccgtgaggca gtttat 276

<210> 68

<211> 248

<212> DNA

<213> Chlamydia

<400> 68

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tatgaaaactt cttctgaaag cgattctgag gcataagaag catttagttt tattcggtt 180  
ttctctttta tccatattag ggctaacgt aacgtctcaa gcagaaattt tttctctagg 240  
tcttattg 248

<210> 69

<211> 715

<212> DNA

<213> Chlamydia

<220>

<221> unsure

<222> (34)

<223> n=A,T,C or G

<400> 69

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attttcatat agtttcgac ggaactctt attaaactcc caaaaccgaa tggtagtcgt 180  
gtgggtatg cctatatggt aaggaggtt ttggcttcg agaatattgg tgatcatttt 240  
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tggtagagcc ggtatagcgc tctagcatgt cacaggcgat tggatcttcg ctgatffff 660  
tatgtttagt ggtcataaat cacagatatt ataatggta gagaatcttt tttc 715

<210> 70

<211> 323

<212> DNA

<213> Chlamydia

<400> 70

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ggagaatcc aacattctct cctgcacgac ttctggag ttctttctg aacatttcaa 180  
ccccagtaac aatcgttct ttagtatctc taagaccgac caactgaact ttatcgaaa 240

ctttaacaat tccacgctca atacgtccag ttactacagt tcctcgccg gagatagaga 300  
acacgtcctc aatgggcatt aag 323

<210> 71  
<211> 715  
<212> DNA  
<213> Chlamydia

<400> 71  
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ggatccgaa ggaatcttcc tttaggagca ctttgcgtga tatcggatct acctt 715

<210> 72  
<211> 641  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (550)  
<223> n=A,T,C or G  
<221> unsure  
<222> (559)  
<223> n=A,T,C or G  
<221> unsure  
<222> (575)  
<223> n=A,T,C or G  
<221> unsure  
<222> (583)  
<223> n=A,T,C or G  
<221> unsure  
<222> (634)  
<223> n=A,T,C or G  
<221> unsure  
<222> (638)  
<223> n=A,T,C or G

<400> 72  
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cctgattctc taccagtcgg cgttccgtca agtttcgata gaaatcttc acaatagcag 180  
gatgataagc gttcgtagtt ctggaaaaga aatctacaga aattcccaat ttcttgaagg 240  
tatctttatg aagcttatga tacatgtcga catattcttgcataccatcgatcgttccact 300  
ctgcattaaag ggttaattgcg attccgtatt catcagaacc acaaataatac aaaaccttcc 360  
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gtccaaaatg caaaggacca tttgcgtaag gcaacgcaga agtaataaga atacgggaag 480  
attccactat ttcacgtcgc tccagttgta cagagaagga tctttcttc tggatgttcc 540  
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tcagcgtatt cgactgatg ccctaaagat cccnggangt t 641

<210> 73  
<211> 584  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (460)  
<223> n=A,T,C or G  
<221> unsure  
<222> (523)  
<223> n=A,T,C or G  
<221> unsure  
<222> (541)  
<223> n=A,T,C or G  
<221> unsure  
<222> (546)  
<223> n=A,T,C or G

<400> 73

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catagccgtg attgatgtac aaggagctt ggctctgaag aagcaaatgc cggcagtcac 240  
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agagaaaagat ttccagaaga aagaagatt agagcatagc gttgtcgaaa ttgtgtccgc 360  
tagcgaattt gattatgttg tggtaatga tgatttgatt acagcatatc aagtttaag 420  
aagtatttt atagctgaag aacataggat gagtcatggm tagaaaagat cgtttaacta 480  
atgaaaagact gaataagcta tttgatagcc ccttttagttt ggntaattac gtaattaagc 540  
nagctnagaa caaaatttgct agaggagat ttcgttcttc taac 584

<210> 74  
<211> 465  
<212> DNA  
<213> Chlamydia

<400> 74

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caatgcggcg tggagtagctg ggtatcggtc tggatggta tggattttct ccattacaca 180  
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<210> 75  
<211> 545  
<212> DNA  
<213> Chlamydia

<400> 75  
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<210> 76  
<211> 797  
<212> DNA  
<213> Chlamydia

<220>  
<221> unsure  
<222> (788)  
<223> n=A,T,C or G  
<221> unsure  
<222> (789)  
<223> n=A,T,C or G

<400> 76  
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tgctttgtct atcaatggat ctccgcaatc taatattaaa ggcactctag gatacgggtga 480  
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attatcccaa tccccgacgtc tcatccagca atcttccatt cgaaagattt ggaatcagat 720  
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<210> 77  
<211> 399  
<212> DNA  
<213> Chlamydia

<400> 77  
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<210> 78
<211> 285
<212> DNA
<213> Chlamydia

<400> 78
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attgtaaaaga aagtttggga atacattaaa aaacacaact gtcaggatca aaaaaataaaa 180
cgtaatatcc ttcccgtgc gaatcttgcc aaagttttg gctctagtga tcctatcgac 240
atgtccaaa tgacccaaagc ccttccaaa catattgtaa aataa 285

<210> 79
<211> 950
<212> DNA
<213> Chlamydia

<400> 79
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cgaggttgcgaa gaaaagataa ccgcctctca aggttttatt ttgtttagat 950

<210> 80
<211> 395
<212> DNA
<213> Chlamydia

<400> 80
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<210> 81
<211> 2085
<212> DNA
<213> Chlamydia

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&lt;400&gt; 81

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&lt;210&gt; 82

&lt;211&gt; 405

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 82

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&lt;210&gt; 83

&lt;211&gt; 379

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

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<212> DNA  
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<210> 87

<211> 3031

**<212> DNA**

<213> Chlamydia

<400> 87

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<211> 976  
<212> DNA  
<213> Chlamydia

<400> 88

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<211> 94  
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<213> Chlamydia

<400> 89

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Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr  
 35 40 45

Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu  
 50 55 60

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Met Phe Gln Met Thr Lys Ala Leu Ser Lys His Ile Val Lys  
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<210> 90  
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 20 25 30

Ala Gln Ala Gly Leu Lys Thr Ala Leu Ile Glu Lys Arg Glu Ala Gly  
 35 40 45

Gly Thr Cys Leu Asn Arg Gly Cys Ile Pro Ser Lys Ala Leu Leu Ala  
 50 55 60

Gly Ala Glu Val Val Thr Gln Ile Arg His Ala Asp Gln Phe Gly Ile  
 65 70 75 80

His Val Glu Gly Phe Ser Ile Asn Tyr Pro Ala Met Val Gln Arg Lys  
 85 90 95

Asp Ser Val Val Arg Ser Ile Arg Asp Gly Leu Asn Gly Leu Ile Arg  
 100 105 110

Ser Asn Lys Ile Thr Val Phe Ser Gly Arg Gly Ser Leu Ile Ser Ser  
 115 120 125

Thr Glu Val Lys Ile Leu Gly Glu Asn Pro Ser Val Ile Lys Ala His  
 130 135 140

Ser Ile Ile Leu Ala Thr Gly Ser Glu Pro Arg Ala Phe Pro Gly Ile  
 145 150 155 160

Pro Phe Ser Ala Glu Ser Pro Arg Ile Leu Cys Ser Thr Gly Val Leu  
 165 170 175  
 Asn Leu Lys Glu Ile Pro Gln Lys Met Ala Ile Ile Gly Gly Val  
 180 185 190  
 Ile Gly Cys Glu Phe Ala Ser Leu Phe His Thr Leu Gly Ser Glu Val  
 195 200 205  
 Ser Val Ile Glu Ala Ser Ser Gln Ile Leu Ala Leu Asn Asn Pro Asp  
 210 215 220  
 Ile Ser Lys Thr Met Phe Asp Lys Phe Thr Arg Gln Gly Leu Arg Phe  
 225 230 235 240  
 Val Leu Glu Ala Ser Val Ser Asn Ile Glu Asp Ile Gly Asp Arg Val  
 245 250 255  
 Arg Leu Thr Ile Asn Gly Asn Val Glu Glu Tyr Asp Tyr Val Leu Val  
 260 265 270  
 Ser Ile Gly Arg Arg Leu Asn Thr Glu Asn Ile Gly Leu Asp Lys Ala  
 275 280 285  
 Gly Val Ile Cys Asp Glu Arg Gly Val Ile Pro Thr Asp Ala Thr Met  
 290 295 300  
 Arg Thr Asn Val Pro Asn Ile Tyr Ala Ile Gly Asp Ile Thr Gly Lys  
 305 310 315 320  
 Trp Gln Leu Ala His Val Ala Ser His Gln Gly Ile Ile Ala Ala Arg  
 325 330 335  
 Asn Ile Gly Gly His Lys Glu Glu Ile Asp Tyr Ser Ala Val Pro Ser  
 340 345 350  
 Val Ile Phe Thr Phe Pro Glu Val Ala Ser Val Gly Leu Ser Pro Thr  
 355 360 365  
 Ala Ala Gln Gln Gln Lys Ile Pro Val Lys Val Thr Lys Phe Pro Phe  
 370 375 380  
 Arg Ala Ile Gly Lys Ala Val Ala Met Gly Glu Ala Asp Gly Phe Ala  
 385 390 395 400  
 Ala Ile Ile Ser His Glu Thr Thr Gln Gln Ile Leu Gly Ala Tyr Val  
 405 410 415  
 Ile Gly Pro His Ala Ser Ser Leu Ile Ser Glu Ile Thr Leu Ala Val  
 420 425 430  
 Arg Asn Glu Leu Thr Leu Pro Cys Ile Tyr Glu Thr Ile His Ala His  
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		30
Gly Ser Ala Arg Ser Asp Glu Ile Ile Lys Lys Leu Lys Leu Asp Pro		
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Glu Ala Arg Ala Ser Glu Leu Thr Glu Glu Glu Val Gly Arg Leu Asn		
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		60
Ser Leu Leu Gln Ser Glu Tyr Thr Val Glu Gly Asp Leu Arg Arg Arg		
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		75
		80
Val Gln Ser Asp Ile Lys Arg Leu Ile Ala Ile His Ser Tyr Arg Gly		
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		95
Gln Arg His Arg Leu Ser Leu Pro Val Arg Gly Gln Arg Thr Lys Thr		
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Lys		
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Ser Leu Ala Asp Phe Arg Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro		
	35	40
		45

Lys Asp Phe Thr Tyr Val Cys Pro Thr Glu Leu His Ala Phe Gln Asp  
50 55 60

Arg Leu Val Asp Phe Glu Glu His Gly Ala Val Val Leu Gly Cys Ser  
65 70 75 80

Val Asp Asp Ile Glu Thr His Ser Arg Trp Leu Thr Val Ala Arg Asp  
85 90 95

Ala Gly Gly Ile Glu Gly Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser  
100 105 110

Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu  
115 120 125

Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His  
130 135 140

Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu  
145 150 155 160

Arg Ile Leu Asp Ser Leu Ile Phe Phe Glu Asn His Gly Met Val Cys  
165 170 175

Pro Ala Asn Trp Arg Ser Gly Glu Arg Gly Met Val Pro Ser Glu Glu  
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Gly Leu Lys Glu Tyr Phe Gln Thr Met Asp  
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<400> 93  
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<210> 94  
<211> 20  
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<220>  
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<400> 94

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<210> 95  
<211> 20  
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<220>  
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<210> 96  
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<210> 97  
<211> 20  
<212> PRT  
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<220>  
<223> Made in a lab

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<210> 98  
<211> 20  
<212> PRT  
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<210> 99  
<211> 16  
<212> PRT  
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<400> 99  
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<210> 100  
<211> 15  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 100  
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<210> 101  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 101  
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<210> 102  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 102  
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Lys Arg Asn Ile  
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<210> 103

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 103

Lys Val Trp Glu Tyr Ile Lys Lys His Asn Cys Gln Asp Gln Lys  
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<210> 104

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 104

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Ser Asp Tyr Val  
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<210> 105

<211> 21

<212> PRT

<213> Artificial Sequence

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<223> Made in a lab

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Ser Asp Ile Lys Arg  
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<210> 106

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 106

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Ile Ser Leu Thr

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<210> 107  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 107  
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Ser Asp Tyr Val  
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<210> 108  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 108  
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<210> 109  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 109  
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<210> 110  
<211> 1461  
<212> DNA  
<213> Chlamydia

<400> 110  
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 tccgcattaa aaataaaaag gggaaaaat gaggactact attagcgag acgttcttc 960  
 tttaccgttg ccaacagctt cctgcgtaga gacaaaatct acttcgtctt caacaaaagg 1020  
 gaatacttgt tccaaaattt tggatatacg ttttagctatc gtggcgctt tagttgtgt 1080  
 cgctgggta ttagcttgg ttttgcgc tagcaatgtc atatttactg taataggtat 1140  
 tcctgcatta attattggat ctgcttgcgtgt ggggtgcggga atatctcgatc ttatgtatcg 1200  
 atccctttat gctagcttag aagaaaaaaaaa tggtttggct gagcaacgatc tgcgtatct 1260  
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 tcttacggac gatctccaag ctggaaagc taaggtaatg gaatttgaga ttgattgttt 1380  
 ggacagatata gaaaaatg agcaagctt attgtccgat gtgcgcttag ttttatctag 1440  
 ctacacaaga tggttggata g 1461

<210> 111  
 <211> 267  
 <212> DNA  
 <213> Chlamydia

<400> 111  
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 acagaattcg tggaggattc cgggttgcg cagttaaagc tccaggcttt ggagatagaa 120  
 gaaaagctat gttggaaagac atcgatctt taactggcg tcaactcatt agcgaagagt 180  
 tggcatgaa attagaaaac gctaacttag tttatgttggaa taaagctaaa aaagttatcg 240  
 tttctaaaga agacacgacc atcgatc 267

<210> 112  
 <211> 698  
 <212> DNA  
 <213> Chlamydia

<400> 112  
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 tggaaaattcc tacgagaagg agctggcatg ctttagaaaag aaacgcgatc gcttacaaaa 120  
 agatctgagc caactgaaaa aatcacacatc tctctacatc aagaagctgc tggaaaccta 180  
 cagacaactc gggcatcgaa agacaaaat tgcaaaaattt gatgacccatc ctaccggag 240  
 agtctccgtc cataagaaaag caaaagaact cgctgcgctc gatcaagaag agaacttcta 300  
 aaacgtgact cggcccttga gatccttaaa ctctcgggcc aaaaagacta cagtcttctc 360  
 gagaagaaaa acgggtttag aaaatacgcg cgcttacact ttctcttaca atgactcaaa 420  
 aagctgtaaa cgtatacgtt taccgctctt ccataatttc taggctgact ttcacattat 480  
 ctcgacttgc tacggaaacc aataaaatgtac ggtatgcctt aatagtgctc ctttcttac 540  
 cgataatttt accgatatct cccttagcaa cagtcaattc gtagataatc gtattggttc 600  
 cctgcacccctc tttcagatgc acttccctcg gcttacac aagatttttt acaatgtacg 660  
 ctaaaaactc tttcatgcga agcaaatcct acacaagc 698

<210> 113  
 <211> 1142  
 <212> DNA

<213> Chlamydia

<400> 113

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aacgaaaaaa gaaggtattt tgattccctc tgcaaggatt gatgaatcga atacggacca 180
gcctttgtt ttatatccta aagatattt ggatcggtt aatcgcatcg gagaatgggt 240
aagaattat ttccgagtga aagagctagg cgtaatcatt acagatagcc atactactcc 300
aatgcggcgt ggagtaactgg gtatcggct gtgttggtat ggatttctc cattacacaa 360
ctatatagga tcgcttagatt gtttcggctcg tcccttacag atgacgaaa gtaatcttgt 420
agatgcctta gcagttgcgg ctgttggttg tatgggagag gggaaatgagc aaacaccgtt 480
agcggtgata gagcaggcac ctaatatgtt ctaccattca tattcctactt ctgcagaaga 540
gtattgttct ttgcycatag atgaaacaga ggacttatac ggaccttt tgcaagcgg 600
tacgtggagt caagaaaaga aatgtggag gtgtttatga attttttaga tcagtttagat 660
ttaatttattc aaaataagca tatgcttagaa cacacgtttt atgtgaaatg gtcaaggggg 720
gagcttacta aagaycaatt acaggcgtat gccaaagact attatttaca tatcaaagcc 780
tttccttaat attatctgc gattcatagt cgttgcgtatg atttagaggc gcgttaagtta 840
ttgttagata acttyatggta tgaagagaac ggttaccctta atcatattga ttgtggaag 900
cagttgtgt ttgctctagg agttactcca gaagagttag aggttcatga gccttagtgaa 960
gcagcaaaag cgaaagtgc tactttcatg cgggtgggtgtc caggagattc tttagctgca 1020
ggagtggctg cttttagttt ttatgagatg caaattccac gtatcgctg agagaaaatt 1080
cgtggattga ctgagttactt tggatttcc aatcctgaag actatgcata ttccacagaa 1140
ca                                         1142

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<210> 114

<211> 976

<212> DNA

<213> Chlamydia

<400> 114

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aggtggatgg ggcgcctgtc caagatgtgc tcgttactct atatggaaagc aatcacaaaag 60
ggactgcgc tgaagagtgc gctgctttaa gaacactatt ctctcgcatg gctcttttag 120
ggcacaaaat accttctggg cgcactactt taaagattcg tcgtcctttt ggtactacga 180
gagaagttcg tggaaatgg cggttatgttc ctgttgcgtt aggagattt gctaccatag 240
ctccttctat cagggtctcca cagttacaga aatcgatgag aagtttttc cctaagaaaag 300
atgatgcgtt tcatcggtct agttcgctat tctactctcc aatggttccg cattttggg 360
cagagttcg caatcattat gcaacgagtg gtttggaaaag cgggtacaat artggagta 420
ccgatgggtt tctccctgtc attgggcctg ttatatggta gtcggagggt ctgttccgcg 480
tttatatttc ttcggtgact gatggggatg gtaagagcca taaagtagga ttcttaagaa 540
ttcctacata tagttggcag gacatggaaat ttgtatcc ttcaaggaccg cttccctggg 600
aagaatttgc taagattatt caagtattt ctcttaatac agaagctttt attatcgacc 660
aaacgaacaa cccaggtggt agtgccttt atctttatgc actgcttcc atgttgcac 720
accgtccctt agaacttcctt aaacatagaa tgattctgac tcaggatgaa gtgggtgtat 780
cttttagattt gtttaccctgt ttggaaaacg tagacacaaa cgtggatgtc cgccttgc 840
ttggagacaa catggaaatg tatactgtgg atctacaggt tgccgagttt taaaaaaagct 900
ttggacgtca agtattgaat tggatggatg aaggggatat cgagttatca acacctattc 960
ctcttttgg ttttga                                         976

```

<210> 115

<211> 995

<212> DNA

<213> Chlamydia

<400> 115

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ttatcctaga aatttgggtt tcaatatgag cgaaaaaaaga aagtctaaaca aaattattgg 60

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tattgcctct tctgaaggaa ctcgtactac tccttctatc gttgtttta aagggtggcga 180  
aactcttgcgtt ggaattcctg caaaaacgtca ggcagtaacc aatcctgaaa aaacattggc 240  
ttctactaag cgattcatcg gtagaaaatt ctctgaagtc gaatctgaaa ttaaaacagt 300  
cccctacaaa gttgtcccta actcgaaagg agatcggtc tttgatgtgg aacaaaaact 360  
gtacactcca gaagaaaatcg ggcgtcagat cctcatgaag atgaaggaaa ctgtgaggc 420  
ttatctcgga gaaacagttaa cggaagcagt cattaccgtc ccagcttact ttaacgattc 480  
tcaaagagct tctacaaaag atgctggacg tatcgagga tttagatgtta aacgcattat 540  
tcctgaacca acagcggccg ctcttgccta tggattgtat aaggaaggag ataaaaaaat 600  
cgccgtttc gacttaggag gaggaacttt cgatatttct atcttgaaa tcgtgacgg 660  
agtttttggaa gttctctcaa ccaacgggaa tactcaatttggggagacy acttcgacgg 720  
agtcatcatc aactggatgc tttagatgaaatt caaaaaacaa gaaggcatttgc atctaagcaa 780  
agataaacatg gcttgaaa gattgaaaga tgctgtgaa aaagcaaaaa tagaattgtc 840  
tgggtgtatcg tctactgaaa tcaatcagcc attcatcaat atcgacgcta atggacctaa 900  
acatttggct ttaactctaa ctcgcgtca attcgaacac ctagcttcct stctcattga 960  
gcgaaccaaa caacccgtg ctcaggcattt aaaag 995

&lt;210&gt; 116

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 116

gtcacagcta aaggcggtgg gcatttatact gataagaatc ttccgattac taacatcaca 60  
ggaattatcg aaattgcaaa taacaaagcg acagatgttg gaggtggtgc ttacgtaaaa 120  
ggaaccctta ctgtaaaaaa ctctcaccgtt ctacaatttt tgaaaaactc ttccgataaa 180  
caaggtggag gaatctacgg agaagacaac atcaccctat ctaattcgac agggaaagact 240  
ctattccaag agaataactgc caaaaaagag ggcgggtggac tcttcataaa aggtacagat 300  
aaagctctta caatgacagg actggatagt ttctgtttaa ttaataacac atcagaaaaaa 360  
catgggtgggaa gggctttgtt taccggaaatc atctctcaga cttacaccc tcgtatgtggaa 420  
acaattccag gaatcac 437

&lt;210&gt; 117

&lt;211&gt; 446

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 117

aagtttaccc agaccaaact gaagatgacg aaggaaaaagt tgtttatcc agagaaaaag 60  
caacaagaca acgacaatgg gaatacattc ttgtctactg cgaggaaggt tctattgtta 120  
agggacaaat taccggaaaa gtttaggggtg gttgtatcgt agatattggat atggaaagcct 180  
tccttccagg atcccaata gacaataaga agatcaagaa ctttagatgtat tacgttaggca 240  
aggtttgtga gttcaaaatt ctcaaaatca acgtggatcg tcggaaacgtt gtgttatcta 300  
gaagagaact tctcgaagct gaacgcattt ctaagaaaagc agagttgtatc gagcaaatca 360  
ctatcggtga acgtcgccaa ggtatcgatc agaatatcac agattcgga gtattcttgg 420  
atcttgcgttga cattgacggc ctactc 446

&lt;210&gt; 118

&lt;211&gt; 951

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 118

agtatttgcga aatattactg tgagaagcaa tgctgagagc ggttctagta aaagtgggg 60  
gagagctgtc agaagggttc gtcagggaaatc cgagacaacg tggtgtatc ttatttaggaa 120

gattccctct ttatccctaa atcgatctgg aaacgctagt ttagtggag actctatgcc 180  
tgaaggggaa atgatgcata agttgcaga tgcatacat agaaaatgtt tggttctcg 240  
tcgttatccc ttctccgaaac ctgttaacggaa gaaaatgtct gcagaagcca tcaaaaagct 300  
ttggtatccg gaactcacca atcctggggca gccaattgtt tttgtcatta atagccctgg 360  
agggtctgtt gatgctgggt ttgctgtttt ggaccggaaatt aaaatgtatct cttctccctt 420  
gactacagtt gttacagggtt tagcagcatc tatggatct gtattgagtt tgtgtctgt 480  
tccaggaaga cgtttgcta cgccctcatgc ggcgcattatg attcaccaggc cttctattgg 540  
aggaaccatt actggcataag ccacggactt ggatattcat gtcgtgaaa ttttaaaaac 600  
aaaagcacgc attattgtat tgcataatgcg ggcaactggaa caatctccag aggtataga 660  
gaaagctatc gatcgagata tgcataatgcg tgcaaatggaa gcaatggagt ttggactgtt 720  
agatgggatt ctcttcctt ttaacgactt gtagatatct ttatattct ggagcaggaa 780  
acagtttcatttttttttggagaa tcgatgcctt ctcttgagga ttttctgttt ttatgccagg 840  
aagagatgtt tgcataatgcg ttatgtgttag agtcttctga aatagcagat gctaaactca 900  
ctgtttttaa taqtqatqqa tctatcqct ctatgtgcgg gaatgggtt c 951

<210> 119  
<211> 953  
<212> DNA  
<213> Chlamydi

<400> 119  
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catcaacacc tgtcgcagcc aaaatgacag cttctgatgg aatatcttta acagtcctca 120  
ataatccatc aaccaatgtc tctattacaa ttggggaga tgcgaaaaaa gcttaccaggc 180  
ttattctaga aaagttggga gatcaaattc ttgggaaat tgctgataact atttgtata 240  
gtacagtcca agatattttt gacaaaatca caacagaccc ttctcttaggt ttgttggaaag 300  
cttttaacaa ctttccaatc actaataaaaa ttcaatgcaa cgggttattc actcccaagga 360  
acattgaaac tttatragga ggaactgaaa tagggaaatt cacagtccaca cccaaagct 420  
ctgggagcat gttcttagtc tcagcagata ttattgcattc aagaatggaa ggccggcggtt 480  
ttctagcttt ggtacgagaa ggtgattcta agccctacgc gatttagttat ggataactcat 540  
caggcgttcc taatttatgt agtctaagaa ccagaattat taatacagga ttgactccgaa 600  
caacgttattc attacgtta ggcgggtttag aaagcggtgt ggtatgggtt aatyccttt 660  
ctaattggca tgatattttt ggaataacaa atacttctaa tttatctttt ttggaggtaa 720  
tacctcaaac aaacgcttaa acaattttt ttggattttt cttataggtt ttatatttag 780  
agaaaaaaagt tcgaattacg gggtttggta tgcaaaataa aagcaaaatg agggacgatt 840  
ttattaaaat tgtaaagat tcctggatc ggtctgcgttccgactctgt ccaacatcaa 900  
tacaacctat taattcccc tcgtcaaaaaa taaggttatc aagtgagaaa tca 953

<210> 120  
<211> 897  
<212> DNA  
<213> Chlamydia

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<400> 120
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gttaaggctcg ccaagtctgc tgccgaattt accgc当地 aaaa ttggaaaca agctggaggc 180
gcgggc当地 ccccacacat tacagctcc caagtgtcca aaggattagg ggatgc当地 240
actgttctcg cttagggaa tgc当地taac ggagcggtgc caggaacagt tcaaagtgc当地 300
caaagcttct tctcttacat gaaagctgct agtc当地aaaac cgcaagaagg ggatgagggg 360
ctcgtacgag atctttgtgt gtctcataag cgcanagcgg ctgc当地ctgt ctgttagctc 420
atcgaggaa ttacctaccc cgacatcc ggagctatcc gtccgattct gtttgc当地ac 480
aaaatgc当地 cgcaaccgtt tctttctcc caaattaaag caaatatggg atcttctgtt 540
agctatatta tggcggctaa ccatgcagcg tttgtgggg gttctggact cgctatcagt 600

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gcggaaagag cagattgcga agcccgctgc gctcgttattg cgagagaaga gtcgtcaactc	660
gaattgtcgg gagaggaaaa tgcttgcgag aggagagtgc ctggagagaa accaagacg	720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agttttgga atgcgttgcc	780
gacgtttca aatttgtgcc gttgcctatt acaatggta ttctgtcaat ttgtggctgcg	840
ggatgtacgt tcacttctgc agttattgga ttgtggactt tctgcgccag agcataa	897

<210> 121  
 <211> 298  
 <212> PRT  
 <213> Chlamydia

<400> 121		
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu		
1	5	10
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn		
20	25	30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala		
35	40	45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser		
50	55	60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg		
65	70	75
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr		
85	90	95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln		
100	105	110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser		
115	120	125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile		
130	135	140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn		
145	150	155
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Ile Lys Ala Asn Met		
165	170	175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val		
180	185	190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala		
195	200	205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly		
210	215	220
Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr		
225	230	235
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu		
245	250	255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met		
260	265	270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val		
275	280	285
Ile Gly Leu Trp Thr Phe Cys Ala Arg Ala		
290	295	

<210> 122  
 <211> 897  
 <212> DNA  
 <213> Chlamydia

&lt;400&gt; 122

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acacagccca	gcaataaaat	ggcaagggt	gttataaga	cgaaggaaat	120
gttaaggctcg	ccaagtctgc	tgccgaattt	accgcaaata	tttggaca	180
gcgggcttctt	ccgcacacat	tacagcttcc	caagtgtcca	aaggattagg	240
actgttgcg	ctttagggaa	tgccttaac	ggagcgttgc	caggaacagt	300
caaagcttct	tctctcacat	gaaagctgt	agttagaaaa	cgcaagaagg	360
ctcacagcag	atcttgcgt	gtctcataag	cgcagagcgg	ctgcggctgt	420
atcggaggaa	ttaccttacct	cgcacattc	ggagttatcc	gtccgattct	480
aaaatgctgg	tgaacccgtt	tctttttcc	caaactaaag	caaatatggg	540
agctatatta	tggcggtctaa	ccatgcagcg	tctgtgggt	gtgctggact	600
gcggaaagag	cagattgcga	agcccgcgtc	gtcgttattt	cgagagaaga	660
gaagtgtcgg	gagagggaaa	tgcttgcgag	aagagagtctg	ctggagagaa	720
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gacgttttca	aatttggtgc	gctgcctatt	acaatggta	ttcgtgcgt	840
ggatgtacgt	tcacttctgc	aattatttgg	ttgtgcactt	tctgcgccag	897

&lt;210&gt; 123

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;400&gt; 123

Met	Ala	Ser	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	Ala	Leu
1				5				10					15		
Lys	Ala	Phe	Phe	Thr	Gln	Pro	Ser	Asn	Lys	Met	Ala	Arg	Val	Val	Asn
					20				25				30		
Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Val	Lys	Val	Ala	Lys	Ser	Ala	Ala
					35			40				45			
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gin	Ala	Gly	Gly	Ala	Gly	Ser	Ser
					50			55			60				
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Thr	Arg
					65			70			75		80		
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr
					85			90			95				
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ser	Gln	
					100			105			110				
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
					115			120			125				
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Gly	Phe	Ile	Gly	Gly	Ile
					130			135			140				
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Val	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
					145			150			155		160		
Lys	Met	Leu	Val	Asn	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
					165			170			175				
Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
					180			185			190				
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Glu	Arg	Ala	Asp	Cys	Glu	Ala
					195			200			205				
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Leu	Leu	Glu	Val	Ser	Gly
					210			215			220				
Glu	Glu	Asn	Ala	Cys	Glu	Lys	Arg	Val	Ala	Gly	Glu	Lys	Ala	Lys	Thr
					225			230			235		240		
Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met	Leu	Glu	Lys	Phe	Leu

245	250	255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met		
260	265	270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile		
275	280	285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala		
290	295	

&lt;210&gt; 124

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 124

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acacagccca acaataaaat ggcaagggtta gtaataaga cgaaggaaat ggataagact	120
attaagggtt ccaagtctgc tgccgaattt accgcaaata ttttggaca agctggagc	180
gccccgtttt ccgcacacat tacagcttcc caagtgtcca aaggattagg gcatgcgaga	240
actgttgtcg cttaggaa tgcctttaac ggagcgttgc caggaacagt tcaaagtgcg	300
caaagcttct tctctcacat gaaagctgct agtcagaaaa cgcaagaagg gcatggggg	360
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atcggaggaa ttacacctt cgcgcacattt ggagctatcc gtccgattct gtttgtcaac	480
aaaatgtctgg caaaaccgtt tccttcttcc caaactaaag caaatatggg atcttctgtt	540
agctatatta tggcgctaa ccatgcagcg tctgtgggg gtgctggact cgctatcgt	600
gccccaaagag cagattgcga agccgcgtgc gctcgattt cgagagaaga gtcgttactc	660
gaagtgcggg gagagaaaaa tgcttgcgag aagaaagtgc ctggagagaa agccaagacg	720
tccacgcgca tcaagtatgc actcctact atgctcgaga agttttggg atgcgttgcc	780
gacgttttca aattgggtcc gctgcctatt acaatgggtt ttctgtgcgt tttggctgct	840
ggatgtacgt tcacttctgc aattatggg ttctgtgcactt tcctgcggcag agcataaa	897

&lt;210&gt; 125

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;400&gt; 125

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu	15	
1	5	10
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn		
20	25	30
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala		
35	40	45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser		
50	55	60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg		
65	70	75
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr		
85	90	95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln		
100	105	110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser		
115	120	125
His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile		
130	135	140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn		

145	150	155	160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met			
165	170	175	
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val			
180	185	190	
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala			
195	200	205	
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly			
210	215	220	
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr			
225	230	235	240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu			
245	250	255	
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met			
260	265	270	
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile			
275	280	285	
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala			
290	295		

&lt;210&gt; 126

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 126

atggcttcta tatgcggacg tttagggct ggtacaggga atgctctaaa agctttttt	60
acacagccca acaataaaat ggcaagggtta gtaataaga cgaaggaaat ggataagact	120
attaagggttgc ccaagtctgc tgccgaattt accgcaaata ttttggaeaca agctggaggc	180
gcccccttc cgcacacat tacagttcc caagtgtcca aaggatttagg ggatgcgaga	240
actgttgtcg cttagggaa tgccttaac ggagcgttgc caggaacagt tcaaagtgcg	300
caaagttct tcctcacat gaaagctgct agtcgaaaaa cgcaagaagg ggatgagggg	360
ctcacagcag atcttggtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc	420
atcgaggaa ttacctactt cgcgacatcc ggagctatcc gtccgattct gttgtcaac	480
aaaatgctgg caaaaccgtt tctttttcc caaactaaag caaatatggg atcttctgtt	540
agctatatta tggcggctaa ccatgcagcg tctgtggact gtgctggact cgctatcagt	600
gcggaaagag cagattgcga agcccgtc gctcgtattt cgagagaaga gtcgttactc	660
gaagtgcgg gagagggaaa tgcttgcgag aagaaagtcg ctggagagaa accaagacg	720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agttttggaa atgcgttgcc	780
gacgtttca aatttggtgc gctgcattt acaatggta ttcgtgcgtat tgcgttgact	840
ggatgtacgt tcacttctgc aattattggaa ttgtgcactt tctgcgccag acataaa	897

&lt;210&gt; 127

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;400&gt; 127

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu			
1	5	10	15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn			
20	25	30	
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala			
35	40	45	
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser			

50	55	60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg		
65	70	75
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr		80
85	90	95
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln		
100	105	110
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser		
115	120	125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile		
130	135	140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn		
145	150	155
Lys Met Leu Ala Lys Prc Phe Leu Ser Ser Gln Thr Lys Ala Asn Met		160
165	170	175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val		
180	185	190
Val Gly Ala Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala		
195	200	205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly		
210	215	220
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr		
225	230	235
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu		240
245	250	255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met		
260	265	270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile		
275	280	285
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala		
290	295	

&lt;210&gt; 128

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 128

atgggttctta tatgtggacg tttagggct ggtacaggga atgctctaaa agctttttt	60
acacagccca gcaataaaat ggcaagggtt gtaaataaga cgaaggaaat ggataagact	120
gttaaggtcg ccaagtctgc tgccgattt accgcaaata ttttggaaaca agctggaggc	180
gcgggctttt ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatacgaga	240
actgttgtcg cttagggaa tgccttaac ggagcggttc caggaacagt tcaaagtgcg	300
caaagcttct tctctcacat gaaagctgtc agtcagaaaa cgcaagaagg ggatgagggg	360
ctcacagcag atctttgtgt gtctcataag cgccagacgg ctgcggctgt ctgtggcttc	420
atcggaggaa ttaccttacct cgccacattt ggagttatcc gtccgattct gtttgtcaac	480
aaaatgtgg tgaaccgtt tcttttttcc caaaactaaag caaatatggg atcttctgtt	540
agctatatta tggcggttaa ccatgcagcg tctgtggtg gtgctggact cgctatcagt	600
gcggaaagag cagattgcga agcccgtgc gctcgtattt cgagagaaga gtcgttactc	660
gaagtgtcg gagagaaaaa tgcttgcag aagagagtgc ctggagagaa agccaagacg	720
ttcacgcga tcaagtatgc actcctcaact atgctcgaga agtttttggaa atgcgttgcc	780
gacgtttca aattggtgcc gtcgcattt acaatggta ttctgtgcgtat tgtggctgct	840
ggatgtacgt tcacttctgc aattatttggaa ttgtgcactt tctgcgccag agcataa	897

&lt;210&gt; 129

<211> 298  
 <212> PRT  
 <213> Chlamydia

<400> 129

Met	Ala	Ser	Ile	Cys	Gly	Arg	Leu	Gly	Ser	Gly	Thr	Gly	Asn	Ala	Leu
1				5				10					15		
Lys	Ala	Phe	Phe	Thr	Gln	Pro	Ser	Asn	Lys	Met	Ala	Arg	Val	Val	Asn
	20						25					30			
Lys	Thr	Lys	Gly	Met	Asp	Lys	Thr	Val	Lys	Val	Ala	Lys	Ser	Ala	Ala
	35				40						45				
Glu	Leu	Thr	Ala	Asn	Ile	Leu	Glu	Gln	Ala	Gly	Gly	Ala	Gly	Ser	Ser
	50					55				60					
Ala	His	Ile	Thr	Ala	Ser	Gln	Val	Ser	Lys	Gly	Leu	Gly	Asp	Thr	Arg
65						70			75			80			
Thr	Val	Val	Ala	Leu	Gly	Asn	Ala	Phe	Asn	Gly	Ala	Leu	Pro	Gly	Thr
	85						90				95				
Val	Gln	Ser	Ala	Gln	Ser	Phe	Phe	Ser	His	Met	Lys	Ala	Ala	Ser	Gln
	100					105				110					
Lys	Thr	Gln	Glu	Gly	Asp	Glu	Gly	Leu	Thr	Ala	Asp	Leu	Cys	Val	Ser
	115				120				125						
His	Lys	Arg	Arg	Ala	Ala	Ala	Ala	Val	Cys	Gly	Phe	Ile	Gly	Gly	Ile
	130					135				140					
Thr	Tyr	Leu	Ala	Thr	Phe	Gly	Val	Ile	Arg	Pro	Ile	Leu	Phe	Val	Asn
145						150			155			160			
Lys	Met	Leu	Val	Asn	Pro	Phe	Leu	Ser	Ser	Gln	Thr	Lys	Ala	Asn	Met
	165					170				175					
Gly	Ser	Ser	Val	Ser	Tyr	Ile	Met	Ala	Ala	Asn	His	Ala	Ala	Ser	Val
	180					185				190					
Val	Gly	Ala	Gly	Leu	Ala	Ile	Ser	Ala	Glu	Arg	Ala	Asp	Cys	Glu	Ala
	195					200			205						
Arg	Cys	Ala	Arg	Ile	Ala	Arg	Glu	Glu	Ser	Leu	Leu	Glu	Val	Ser	Gly
	210					215			220						
Glu	Glu	Asn	Ala	Cys	Glu	Lys	Arg	Val	Ala	Gly	Glu	Lys	Ala	Lys	Thr
225						230			235			240			
Phe	Thr	Arg	Ile	Lys	Tyr	Ala	Leu	Leu	Thr	Met	Ile	Glu	Lys	Phe	Leu
	245						250				255				
Glu	Cys	Val	Ala	Asp	Val	Phe	Lys	Leu	Val	Pro	Leu	Pro	Ile	Thr	Met
	260					265			270						
Gly	Ile	Arg	Ala	Ile	Val	Ala	Ala	Gly	Cys	Thr	Phe	Thr	Ser	Ala	Ile
	275					280			285						
Ile	Gly	Leu	Cys	Thr	Phe	Cys	Ala	Arg	Ala						
	290					295									

<210> 130  
 <211> 897  
 <212> DNA  
 <213> Chlamydia

<400> 130

atggctgcta	tatgtggacg	tttagggtct	ggtacaggga	atgctctaaa	agcttttttt	60
acacagccca	gcaataaaat	ggcaagggtta	gtaaaataaga	cgaaggaaat	ggataagact	120
gttaagggtcg	ccaagtctgc	tgccgaattt	accgcaaata	ttttggaaaca	agctggaggc	180
gcgggctt	ccgcacacat	tacagttcc	caagtgtcca	aaggattagg	ggatgcgaga	240
actgttctcg	ctttagggaa	tgccttaac	ggagcggtgc	caggaacagt	tcaaagtgcg	300

caaagttct tctttacat gaaagctgct agtcagaaac cgcaagaagg gnatggggg	360
ctcgtagcag atcttgcgt gtctcataag cgcagagcgg ctgcggctgt ctgtatctc	420
atccggaggaa ttacctacct cgcgacattc ggagctatcc gtccgattct gtttgtcaac	480
aaaatgtgg cgcaaccgtt tcttttcc caaactaaag caaatatggg atcttctgtt	540
agctatatta tggcggctaa ccatgcagcg tttgtgggg gttctggact cgctatcagt	600
gcccggaaagag cagattgcga agccccgtgc gctcgtattt cgagagaaga gtcgtcactc	660
gaatttgtcg gaggagaaaa tgcttgcag agggggatcg ctggagagaa agccaagacg	720
ttaacgcgca tcaagtatgc actcctcaact atgctcgaga agtttttggaa atgcgttgcc	780
gacgtttca aattgggtgcc gttgcattt acaatgggtt ttcgtcaat tgtggctgct	840
ggatgtacgt tcacttctgc agttattggaa ttgtggactt ttcgtcaacag agtataa	897

<210> 131  
 <211> 298  
 <212> PRT  
 <213> Chlamydia

<400> 131		
Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu	10	15
1 5		
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn	20	25
20 25		30
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala	35	40
35 40		45
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser	50	55
50 55		60
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg	65	70
65 70		75
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr	85	90
85 90		95
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln	100	105
100 105		110
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser	115	120
115 120		125
His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile	130	135
130 135		140
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn	145	150
145 150		155
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met	165	170
165 170		175
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val	180	185
180 185		190
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala	195	200
195 200		205
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly	210	215
210 215		220
Glu Glu Asn Ala Cys Glu Arg Gly Val Ala Gly Glu Lys Ala Lys Thr	225	230
225 230		235
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu	245	250
245 250		255
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met	260	265
260 265		270
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val	275	280
275 280		285
Ile Gly Leu Trp Thr Phe Cys Asn Arg Val	290	

<210> 132  
<211> 897  
<212> DNA  
<213> Chlamydia

<400> 132

atggctgcta tatgcggacg	tttagggtct ggtacaggga	atgctctaaa agctttttt	60
acacagccca gcaataaaaat	ggcaagggtta gtaaataaga	cgaagggaat ggataagact	120
gttaaggtcg ccaagtctgc	tgcgcatttgc accgcaaata	tttggaaaca agtggaggc	180
gcgggctctt ccgcacacat	tacagttcc caagtgtcca	aaggattagg ggatgcgaga	240
actgttctcg cttagggaa tgccttaac	ggagcgttgc caggaacagt	tcaaagtgcg	300
caaagcttct tctcttacat	gaaagctgtc agtcagaaac	cqcaagaagg ggatgagggg	360
ctcgtagcag atctttgtgt	gtctcatatagg cgccagagcgg	ctgcggctgt ctgtatcttc	420
atcgaggaa ttacatcacct	cgccgacattc ggagctatcc	gtccgattct gtttgtcaac	480
aaaatgctgg cgcaaccgtt	tctttttcc caaactaaag	caaatatggg atcttctgtt	540
agctatatta tggcggctaa	ccatgcagcg tttgttgtgg	gttctggact cgctatcagt	600
gcggaaagcg cagattgcga	agcccgtgc gctcgtattt	cgagagaaga gtcgtcactc	660
gaattgtcgg gagagggaaa	tgcttgtgag aggagagtgc	ctggagagaa accaagacg	720
ttcacgcgca tcaagtatgc	actcctcaact atgctcgaga	agtttttggaa atgcgttgcc	780
gacgtttca aatttgggcc	gttgccattt acaatgggtt	ttcgtgcaat tggcgtgcg	840
ggatgtacgt tcacttctgc	agtttatggta ttgtggactt	tctgcaacag agtataa	897

<210> 133  
<211> 298  
<212> PRT  
<213> Chlamydia

<400> 133

Met Ala Ala Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu			
1	5	10	15
Lys Ala Phe Phe Thr Gln Pro Ser Asn Lys Met Ala Arg Val Val Asn			
20	25	30	
Lys Thr Lys Gly Met Asp Lys Thr Val Lys Val Ala Lys Ser Ala Ala			
35	40	45	
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Ala Gly Ser Ser			
50	55	60	
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg			
65	70	75	80
Thr Val Leu Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr			
85	90	95	
Val Gln Ser Ala Gln Ser Phe Phe Ser Tyr Met Lys Ala Ala Ser Gln			
100	105	110	
Lys Pro Gln Glu Gly Asp Glu Gly Leu Val Ala Asp Leu Cys Val Ser			
115	120	125	
His Lys Arg Arg Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile			
130	135	140	
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn			
145	150	155	160
Lys Met Leu Ala Gln Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met			
165	170	175	
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Phe Val			
180	185	190	
Val Gly Ser Gly Leu Ala Ile Ser Ala Glu Arg Ala Asp Cys Glu Ala			
195	200	205	

Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Ser Leu Glu Leu Ser Gly  
 210 215 220  
 Glu Glu Asn Ala Cys Glu Arg Arg Val Ala Gly Glu Lys Ala Lys Thr  
 225 230 235 240  
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu  
 245 250 255  
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met  
 260 265 270  
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Val  
 275 280 285  
 Ile Gly Leu Trp Thr Phe Cys Asn Arg Val  
 290 295

<210> 134  
<211> 897  
<212> DNA  
<213> Chlamydia

<400> 134  
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acacagccca acaataaaat ggcaagggtta gtaaaaaga cgaaggaaat ggataagact 120  
attaagggttgc ccaagtctgc tgccgaattt accgcaaata ttgttggaca agctggaggc 180  
gcgggcttgc ccgcacacat tacagcttcc caagtgtcca aaggattagg ggatycgaga 240  
actgttgtcg cttagggaa tgcccttaac ggagcgttgc caggaacagt tcaaagtgcg 300  
caaagcttct tctctcacat gaaagctgtc agtcagaaaaa cgcaagaagg ggatggggg 360  
ctcacagcag atctttgtgt gtctcataag cgcatcgcc ctgcggctgt ctgtacatc 420  
atcgaggaa ttacctaccc cgcacattt ggagctatcc gtccgattct gtttgtcaac 480  
aaaatgtcg caaaaccgtt tctttttcc caaactaaag caaatatggg atcttctgtt 540  
agctatattt tggcgctaa ccatgcagcg tctgtgggg gtgctggact cgctatcagt 600  
gcggaaagag cagattgcga agccgcgtgc gctcgatattt cgagagaaga gtcgttactc 660  
gaaaatgccgg gagagaaaaa tgcttgcag aagaaaagtgc ctggagagaa agccaagacg 720  
ttcacgcgc tcaagtatgc actctcaat atgctcgaga agtttttggg atgcgttgcc 780  
gacgtttca aattgggtgcc gctgcctatt acaatgggtt ttcgtgcgt tttggctgtc 840  
ggatgtacgt tcacttctgc aattattggg ttgtgcacct tctgcgccag agcataaa 897

<210> 135  
<211> 298  
<212> PRT  
<213> Chlamydia

<400> 135  
Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu  
1 5 10 15  
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn  
20 25 30  
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala  
35 40 45  
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser  
50 55 60  
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg  
65 70 75 80  
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr  
85 90 95  
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln  
100 105 110

<210> 136  
<211> 882  
<212> DNA  
<213> Chlamydia

<400> 136

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acgcgtcccg gtaacaagct atcacggtt gtaaatagcg caaaaggatt agacagatca	120
ataaagggtt ggaagtctgc tgctgaatta acggcgagta ttttagagca aactgggggg	180
gcagggactg atgcacatgt tacggcgccc aagggtgtca aagcaacttg ggacgcgcga	240
acagtaatgg ctctaggaa tgtcttcaat gggctgtgc cagcaaccat tcaaagtgcg	300
cgaagctgtc tcgcccattt acgagcgccc ggcaaaaag aagaacatcg ctccaagggtg	360
aaagatctct gtgtttctca tagacgaaga gctgcggctg aggcttgtaa tgttatttgg	420
ggagcaacct atattacaac ttccggagcg attcgccga cattactcgt taacaagctt	480
cttgccaaac cattcccttc ctccccaaagcc aaagaagggt tggagcttc tgttgttat	540
atcatggcag cgaaccatgc ggcatctgt ctgggtctg cttaaagtat tagcgcagaa	600
agagcagact gtgaagagcg gtgtgatcgc attcgatgtt gtgaggatgg taaaatttgc	660
gaaggcaata aattaacagc tatttcggaa gagaaggcta gatcatggac tctcatattaag	720
tacagattcc ttactatgtt agaaaaacta tttgagatgg tggcgatat cttcaagttt	780
attccttgc caatttcgca tggattcgt gctattgtt ctgcggatg tacgttgact	840
tctqcaqta ttqgcttaqq tacttttgg tctaqaqcat aa	882

<210> 137  
<211> 293  
<212> PRT  
<213> Chlamydia

<400> 137

Met Ala Ser Val Cys Gly Arg Leu Ser Ala Gly Val Gly Asn Arg Phe  
1 5 10 15

Asn Ala Phe Phe Thr Arg Pro Gly Asn Lys Leu Ser Arg Phe Val Asn  
 20 25 30  
 Ser Ala Lys Gly Leu Asp Arg Ser Ile Lys Val Gly Lys Ser Ala Ala  
 35 40 45  
 Glu Leu Thr Ala Ser Ile Leu Glu Gln Thr Gly Gly Ala Gly Thr Asp  
 50 55 60  
 Ala His Val Thr Ala Ala Lys Val Ser Lys Ala Leu Gly Asp Ala Arg  
 65 70 75 80  
 Thr Val Met Ala Leu Gly Asn Val Phe Asn Gly Ser Val Pro Ala Thr  
 85 90 95  
 Ile Gln Ser Ala Arg Ser Cys Leu Ala His Leu Arg Ala Ala Gly Lys  
 100 105 110  
 Glu Glu Glu Thr Cys Ser Lys Val Lys Asp Leu Cys Val Ser His Arg  
 115 120 125  
 Arg Arg Ala Ala Ala Glu Ala Cys Asn Val Ile Gly Gly Ala Thr Tyr  
 130 135 140  
 Ile Thr Thr Phe Gly Ala Ile Arg Pro Thr Leu Leu Val Asn Lys Leu  
 145 150 155 160  
 Leu Ala Lys Pro Phe Leu Ser Ser Gln Ala Lys Glu Gly Leu Gly Ala  
 165 170 175  
 Ser Val Gly Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val Leu Gly  
 180 185 190  
 Ser Ala Leu Ser Ile Ser Ala Glu Arg Ala Asp Cys Glu Glu Arg Cys  
 195 200 205  
 Asp Arg Ile Arg Cys Ser Glu Asp Gly Glu Ile Cys Glu Gly Asn Lys  
 210 215 220  
 Leu Thr Ala Ile Ser Glu Glu Lys Ala Arg Ser Trp Thr Leu Ile Lys  
 225 230 235 240  
 Tyr Arg Phe Leu Thr Met Ile Glu Lys Leu Phe Glu Met Val Ala Asp  
 245 250 255  
 Ile Phe Lys Leu Ile Pro Leu Pro Ile Ser His Gly Ile Arg Ala Ile  
 260 265 270  
 val Ala Ala Gly Cys Thr Leu Thr Ser Ala Val Ile Gly Leu Gly Thr  
 275 280 285  
 Phe Trp Ser Arg Ala  
 290

&lt;210&gt; 138

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 138

Asp Leu Cys Val Ser His Lys Arg Arg Ala Ala Ala Ala Val Cys Ser  
 1 5 10 15

&lt;210&gt; 139

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Made in a lab

<400> 139

Arg Ala Ala Ala Ala Val Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu  
1 5 10 15

<210> 140

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 140

Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile  
1 5 10 15

Arg Pro

<210> 141

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 14

Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn Lys  
1 5 10 15

Met Leu

<210> 142

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 142

Arg Pro Ile Leu Phe Val Asn Lys Met Leu Ala Gln Pro Phe Leu Ser  
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Ser Gln

<210> 143

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

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Ser

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<220>  
<223> Made in a lab

<400> 144  
Cys Ser Phe Ile Gly Gly Ile Thr Tyr Leu  
1 5 10

<210> 145  
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<220>  
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<210> 146  
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<220>  
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<210> 147  
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<220>  
<223> Made in a lab

<400> 147  
Cys Ser Phe Ile Gly Gly Ile Thr Tyr  
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<210> 148  
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<220>  
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<400> 148  
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<210> 149  
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<220>  
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<400> 149  
Cys Ser Ile Ile Gly Gly Ile Thr Tyr Leu  
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<220>  
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<210> 151  
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<220>  
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<210> 152  
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<210> 153  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
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<210> 154  
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<213> Artificial Sequence

<220>  
<223> Made in a lab

<210> 155  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 155  
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<210> 156  
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<212> PRT  
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<220>

<223> Made in a lab

<400> 156

Leu Ser Thr Lys Cys Trp Arg Asn Arg Phe Phe Leu Pro Lys Leu Lys  
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<210> 157

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 157

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Ser Ser Glu Glu Leu Pro Thr Ser Arg His Ser Glu Leu Ser Val Arg  
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Leu Lys Gln Ile Trp  
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<210> 158

<211> 52

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 158

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Ile Gly Gly Ile Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile  
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35 40 45  
Lys Ala Asn Met  
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<210> 159

<211> 24

<212> DNA

<213> Chlamydia

<400> 159

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24

<210> 160

<211> 24

<212> DNA

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<212> PRT  
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<220>  
 <223> Made in a lab

<400> 167

Ser Phe Ile Gly Gly Ile Thr Tyr Leu  
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<210> 168  
 <211> 9  
 <212> PRT  
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<220>  
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<400> 168

Ser Ile Ile Gly Gly Ile Thr Tyr Leu  
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<210> 169  
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 <212> DNA  
 <213> Chlamydia

<400> 169

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&lt;210&gt; 170

&lt;211&gt; 2949

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

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<210> 171

<211> 2895

<212> DNA

<213> Chlawydia

<400> 171

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<213> Chlamydia

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 Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu Gln Ser  
 515 520 525  
 His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly Tyr Gln  
 530 535 540  
 Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His Ser Leu  
 545 550 555 560  
 Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu Arg Gln  
 565 570 575  
 Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp Met Gln

580	585	590
Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly	Ala Tyr Leu	
595	600	605
Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val His Asp		
610	615	620
Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu Gly Tyr		
625	630	635
Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe Cys Leu		
645	650	655
Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile Thr Ser		
660	665	670
Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu Ala Thr		
675	680	685
Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser Ile His		
690	695	700
Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe Gly Ser		
705	710	715
Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile Pro Ile		
725	730	735
Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe Ser Lys		
740	745	750
Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser Ser Gly		
755	760	765
Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser Leu Pro		
770	775	780
Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr Tyr Tyr		
785	790	795
Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val Glu Ser		
805	810	815
Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala Pro Met		
820	825	830
Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn Gln Arg		
835	840	845
Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val Leu Arg		
850	855	860
Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr Arg Phe		
865	870	880

&lt;210&gt; 176

&lt;211&gt; 982

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(982)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 176

Met Ile Pro Gln Gly Ile Tyr Asp Gly Glu Thr Leu Thr Val Ser Phe		
1	5	10
Pro Tyr Thr Val Ile Gly Asp Pro Ser Gly Thr Thr Val Phe Ser Ala		
20	25	30
Gly Glu Leu Thr Leu Lys Asn Leu Asp Asn Ser Ile Ala Ala Leu Pro		
35	40	45

Leu Ser Cys Phe Gly Asn Leu Leu Gly Ser Phe Thr Val Leu Gly Arg  
 50 55 60  
 Gly His Ser Leu Thr Phe Glu Asn Ile Arg Thr Ser Thr Asn Gly Ala  
 65 70 75 80  
 Ala Leu Ser Asn Ser Ala Ala Asp Gly Leu Phe Thr Ile Glu Gly Phe  
 85 90 95  
 Lys Glu Leu Ser Phe Ser Asn Cys Asn Ser Leu Leu Ala Val Leu Pro  
 100 105 110  
 Ala Ala Thr Thr Asn Lys Gly Ser Gln Thr Pro Thr Thr Ser Thr  
 115 120 125  
 Pro Ser Asn Gly Thr Ile Tyr Ser Lys Thr Asp Leu Leu Leu Asn  
 130 135 140  
 Asn Glu Lys Phe Ser Phe Tyr Ser Asn Leu Val Ser Gly Asp Gly Gly  
 145 150 155 160  
 Ala Ile Asp Ala Lys Ser Leu Thr Val Gln Gly Ile Ser Lys Leu Cys  
 165 170 175  
 Val Phe Gln Glu Asn Thr Ala Gin Ala Asp Gly Gly Ala Cys Gln Val  
 180 185 190  
 Val Thr Ser Phe Ser Ala Met Ala Asn Glu Ala Pro Ile Ala Phe Val  
 195 200 205  
 Ala Asn Val Ala Gly Val Arg Gly Gly Ile Ala Ala Val Gln Asp  
 210 215 220  
 Gly Gln Gln Gly Val Ser Ser Ser Thr Ser Thr Glu Asp Pro Val Val  
 225 230 235 240  
 Ser Phe Ser Arg Asn Thr Ala Val Glu Phe Asp Gly Asn Val Ala Arg  
 245 250 255  
 Val Gly Gly Ile Tyr Ser Tyr Gly Asn Val Ala Phe Leu Asn Asn  
 260 265 270  
 Gly Lys Thr Leu Phe Leu Asn Asn Val Ala Ser Pro Val Tyr Ile Ala  
 275 280 285  
 Ala Lys Gln Pro Thr Ser Gly Gln Ala Ser Asn Thr Ser Asn Asn Tyr  
 290 295 300  
 Gly Asp Gly Gly Ala Ile Phe Cys Lys Asn Gly Ala Gln Ala Gly Ser  
 305 310 315 320  
 Asn Asn Ser Gly Ser Val Ser Phe Asp Gly Glu Gly Val Val Phe Phe  
 325 330 335  
 Ser Ser Asn Val Ala Ala Gly Lys Gly Ala Ile Tyr Ala Lys Lys  
 340 345 350  
 Leu Ser Val Ala Asn Cys Gly Pro Val Gln Phe Leu Arg Asn Ile Ala  
 355 360 365  
 Asn Asp Gly Gly Ala Ile Tyr Leu Gly Glu Ser Gly Glu Leu Ser Leu  
 370 375 380  
 Ser Ala Asp Tyr Gly Asp Ile Ile Phe Asp Gly Asn Leu Lys Arg Thr  
 385 390 395 400  
 Ala Lys Glu Asn Ala Ala Asp Val Asn Gly Val Thr Val Ser Ser Gln  
 405 410 415  
 Ala Ile Ser Met Gly Ser Gly Gly Lys Ile Thr Thr Leu Arg Ala Lys  
 420 425 430  
 Ala Gly His Gln Ile Leu Phe Asn Asp Pro Ile Glu Met Ala Asn Gly  
 435 440 445  
 Asn Asn Gln Pro Ala Gln Ser Ser Lys Leu Leu Lys Ile Asn Asp Gly  
 450 455 460  
 Glu Gly Tyr Thr Gly Asp Ile Val Phe Ala Asn Gly Ser Ser Thr Leu  
 465 470 475 480  
 Tyr Gln Asn Val Thr Ile Glu Gln Gly Arg Ile Val Leu Arg Glu Lys

485	490	495
Ala Lys Leu Ser Val Asn Ser Leu Ser Gln Thr Gly Gly Ser Leu Tyr		
500	505	510
Met Glu Ala Gly Ser Thr Leu Asp Phe Val Thr Pro Gln Pro Pro Gln		
515	520	525
Gln Pro Pro Ala Ala Asn Gln Leu Ile Thr Leu Ser Asn Leu His Leu		
530	535	540
Ser Leu Ser Ser Leu Leu Ala Asn Asn Ala Val Thr Asn Pro Pro Thr		
545	550	555
Asn Pro Pro Ala Gln Asp Ser His Pro Ala Val Ile Gly Ser Thr Thr		
565	570	575
Ala Gly Ser Val Thr Ile Ser Gly Pro Ile Phe Phe Glu Asp Leu Asp		
580	585	590
Asp Thr Ala Tyr Asp Arg Tyr Asp Trp Leu Gly Ser Asn Gln Lys Ile		
595	600	605
Asn Val Leu Lys Leu Gln Leu Gly Thr Lys Pro Pro Ala Asn Ala Pro		
610	615	620
Ser Asp Leu Thr Leu Gly Asn Glu Met Pro Lys Tyr Gly Tyr Gln Gly		
625	630	635
Ser Trp Lys Leu Ala Trp Asp Pro Asn Thr Ala Asn Asn Gly Pro Tyr		
645	650	655
Thr Leu Lys Ala Thr Trp Thr Lys Thr Gly Tyr Asn Pro Gly Pro Glu		
660	665	670
Arg Val Ala Ser Leu Val Pro Asn Ser Leu Trp Gly Ser Ile Leu Asp		
675	680	685
Ile Arg Ser Ala His Ser Ala Ile Gln Ala Ser Val Asp Gly Arg Ser		
690	695	700
Tyr Cys Arg Gly Leu Trp Val Ser Gly Val Ser Asn Phe Phe Tyr His		
705	710	715
Asp Arg Asp Ala Leu Gly Gln Gly Tyr Arg Tyr Ile Ser Gly Gly Tyr		
725	730	735
Ser Leu Gly Ala Asn Ser Tyr Phe Gly Ser Ser Met Phe Gly Leu Ala		
740	745	750
Phe Thr Glu Val Phe Gly Arg Ser Lys Asp Tyr Val Val Cys Arg Ser		
755	760	765
Asn His His Ala Cys Ile Gly Ser Val Tyr Leu Ser Thr Gln Gln Ala		
770	775	780
Leu Cys Gly Ser Tyr Leu Phe Gly Asp Ala Phe Ile Arg Ala Ser Tyr		
785	790	795
Gly Phe Gly Asn Gln His Met Lys Thr Ser Tyr Thr Phe Ala Glu Glu		
805	810	815
Ser Asp Val Arg Trp Asp Asn Asn Cys Leu Ala Gly Glu Ile Gly Ala		
820	825	830
Gly Leu Pro Ile Val Ile Thr Pro Ser Lys Leu Tyr Leu Asn Glu Leu		
835	840	845
Arg Pro Phe Val Gln Ala Glu Phe Ser Tyr Ala Asp His Glu Ser Phe		
850	855	860
Thr Glu Glu Gly Asp Gln Ala Arg Ala Phe Lys Ser Gly His Leu Leu		
865	870	875
Asn Leu Ser Val Pro Val Gly Val Lys Phe Asp Arg Cys Ser Ser Thr		
885	890	895
His Pro Asn Lys Tyr Ser Phe Met Ala Ala Tyr Ile Cys Asp Ala Tyr		
900	905	910
Arg Thr Ile Ser Gly Thr Glu Thr Thr Leu Leu Ser His Gln Glu Thr		
915	920	925

Trp Thr Thr Asp Ala Phe His Leu Ala Arg His Gly Val Val Val Arg  
 930 935 940  
 Gly Ser Met Tyr Ala Ser Leu Thr Ser Asn Ile Glu Val Tyr Gly His  
 945 950 955 960  
 Gly Arg Tyr Glu Tyr Arg Asp Ala Ser Arg Gly Tyr Gly Leu Ser Ala  
 965 970 975  
 Gly Ser Lys Val Xaa Phe  
 980

&lt;210&gt; 177

&lt;211&gt; 964

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

<400> 177  
 Met Lys Ala Phe Phe Phe Leu Ile Gly Asn Ser Leu Ser Gly  
 1 5 10 15  
 Leu Ala Arg Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val  
 20 25 30  
 Pro Asp Pro Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly  
 35 40 45  
 Asp Thr His Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile  
 50 55 60  
 Leu Ala Ile Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile  
 65 70 75 80  
 Thr Asp Tyr Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe  
 85 90 95  
 Ala Lys Asn Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser  
 100 105 110  
 Pro Asn Ser Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile  
 115 120 125  
 Phe Glu Asn Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr  
 130 135 140  
 Ala Ala Asp Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu  
 145 150 155 160  
 Tyr Ile Asn His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser  
 165 170 175  
 Tyr Val Gln Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser  
 180 185 190  
 Glu Asn Gln Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr  
 195 200 205  
 Asn Thr Ala Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser  
 210 215 220  
 Phe Glu Ser Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys  
 225 230 235 240  
 Ala Gly Gly Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg  
 245 250 255  
 Gly Asn Ile Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr  
 260 265 270  
 Ala Ser Ser Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg  
 275 280 285  
 Leu Asp Val Thr Gly Asn Arg Gly Arg Ile Phe Ser Asp Asn Ile  
 290 295 300  
 Thr Lys Asn Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val  
 305 310 315 320

Asp Asn Gly Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly  
                   325                  330                  335  
 Gly Ala Ile Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp  
                   340                  345                  350  
 Arg His Ala Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn  
                   355                  360                  365  
 Ala Asn Gly Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile  
                   370                  375                  380  
 Thr Val Ala Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser  
                   385                  390                  395                  400  
 Gln Asn Leu Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val  
                   405                  410                  415  
 Ser Val Ser Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe  
                   420                  425                  430  
 Ser Gly Ala Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln  
                   435                  440                  445  
 Thr Lys Thr Prc Ala Pro Leu Thr Leu Ser Asn Gln Phe Leu Cys Ile  
                   450                  455                  460  
 Glu Asp His Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly  
                   465                  470                  475                  480  
 Val Val Ser Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly  
                   485                  490                  495  
 Thr Gly Asp Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly  
                   500                  505                  510  
 Leu Asn Leu Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu  
                   515                  520                  525  
 Trp Val Glu Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala  
                   530                  535                  540  
 Ala Thr Phe Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr  
                   545                  550                  555                  560  
 Gly Asn Ser Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser  
                   565                  570                  575  
 Gln Pro Met Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser  
                   580                  585                  590  
 Glu Asn Ile Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln  
                   595                  600                  605  
 Gly Leu Trp Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala  
                   610                  615                  620  
 Ser Ser Ala Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg  
                   625                  630                  635                  640  
 Thr Leu Leu Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys  
                   645                  650                  655  
 His Arg Ser Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu  
                   660                  665                  670  
 Ala Thr Glu Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His  
                   675                  680                  685  
 Pro Phe Trp Gly Ile Thr Gly Gly Leu Gly Met Met Val Tyr Gln  
                   690                  695                  700  
 Asp Pro Arg Glu Asn His Pro Gly Phe His Met Arg Ser Ser Gly Tyr  
                   705                  710                  715                  720  
 Ser Ala Gly Met Ile Ala Gly Gln Thr His Thr Phe Ser Leu Lys Phe  
                   725                  730                  735  
 Ser Gln Thr Tyr Thr Lys Leu Asn Glu Arg Tyr Ala Lys Asn Asn Val  
                   740                  745                  750  
 Ser Ser Lys Asn Tyr Ser Cys Gln Gly Glu Met Leu Phe Ser Leu Gln

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755	760	765
Glu Gly Phe Leu Leu Thr Lys Leu Val Gly Leu Tyr Ser Tyr Gly Asp		
770	775	780
His Asn Cys His His Phe Tyr Thr Gln Gly Glu Asn Leu Thr Ser Gln		
785	790	795
Gly Thr Phe Arg Ser Gln Thr Met Gly Gly Ala Val Phe Phe Asp Leu		
805	810	815
Pro Met Lys Pro Phe Gly Ser Thr His Ile Leu Thr Ala Pro Phe Leu		
820	825	830
Gly Ala Leu Gly Ile Tyr Ser Ser Leu Ser His Phe Thr Glu Val Gly		
835	840	845
Ala Tyr Pro Arg Ser Phe Ser Thr Lys Thr Pro Leu Ile Asn Val Leu		
850	855	860
Val Pro Ile Gly Val Lys Gly Ser Phe Met Asn Ala Thr His Arg Pro		
865	870	875
Gln Ala Trp Thr Val Glu Leu Ala Tyr Gln Pro Val Leu Tyr Arg Gln		
885	890	895
Glu Pro Gly Ile Ala Thr Gln Leu Leu Ala Ser Lys Gly Ile Trp Phe		
900	905	910
Gly Ser Gly Ser Pro Ser Ser Arg His Ala Met Ser Tyr Lys Ile Ser		
915	920	925
Gln Gln Thr Gln Pro Leu Ser Trp Leu Thr Leu His Phe Gln Tyr His		
930	935	940
Gly Phe Tyr Ser Ser Ser Thr Phe Cys Asn Tyr Leu Asn Gly Glu Ile		
945	950	955
Ala Leu Arg Phe		

<210> 178  
<211> 1530  
<212> PRT  
<213> Chlamydia

	165	170	175
Leu Ile Phe Glu Lys Ile Lys Gly Gly	Leu Glu Phe Ala Ser Cys Ser		
180	185	190	
Ser Leu Glu Gln Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His			
195	200	205	
Asp Cys Gln Gly Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala			
210	215	220	
Glu Gly Ser Ser Ala Asn Asp His Leu Gly Phe Gly Gly Ala Phe			
225	230	235	240
Phe Val Thr Gly Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala			
245	250	255	
Gly Asp Met Val Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly			
260	265	270	
Asn Ser Ala Asn Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys			
275	280	285	
Val Leu Phe Val Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg			
290	295	300	
Ala Leu Ser Gly Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln			
305	310	315	320
Asn Cys Ala Glu Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu			
325	330	335	
Asp Lys Gly Ser Leu Gly Gly Ala Ile Ser Ser Leu Gly Thr Val			
340	345	350	
Leu Leu Gln Gly Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala			
355	360	365	
Ser Gln Gly Gly Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn			
370	375	380	
Glu Gly Pro Val Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly			
385	390	395	400
Ala Ile Ala Ala Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly			
405	410	415	
Ile Ser Phe Glu Gly Gly Lys Ala Ser Phe Gly Gly Ile Ala Cys			
420	425	430	
Gly Ser Phe Ser Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp			
435	440	445	
Ile Ser Lys Asn Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr			
450	455	460	
Thr Ser Asp Leu Gly Gln Met Glu Tyr Gln Gly Gly Ala Leu Phe			
465	470	475	480
Gly Glu Asn Ile Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys			
485	490	495	
Asp Asn Ile Val Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly			
500	505	510	
Gly Ala Ile Leu Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly			
515	520	525	
Gly Ile Ser Phe Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr			
530	535	540	
Gln Glu Glu Phe Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser			
545	550	555	560
Ser Gly Tyr Ser Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile			
565	570	575	
Leu His Asn Ala Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser			
580	585	590	
Glu Glu Glu Ala Thr Leu Leu Gly Cys Cys Gly Gly Ala Val His			
595	600	605	

Gly Met Asp Ser Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly  
 610 615 620  
 Asn Asn Tyr Ala Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser  
 625 630 635 640  
 Lys Thr Val Gln Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn  
 645 650 655  
 Ile Ala Ser Leu Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys  
 660 665 670  
 Glu Leu Val Asp Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg  
 675 680 685  
 Val Tyr Gly Gly Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser  
 690 695 700  
 Gly Asn Lys Gly Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu  
 705 710 715 720  
 Tyr Val Glu Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro  
 725 730 735  
 Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln  
 740 745 750  
 Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly  
 755 760 765  
 Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg  
 770 775 780  
 Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala Lys Arg Val Arg Ile Val  
 785 790 795 800  
 Asp Asn Gln Glu Ala Val Val Phe Ser Asn Asn Phe Ser Asp Ile Tyr  
 805 810 815  
 Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg Glu Glu Asp Lys Leu Asp  
 820 825 830  
 Gly Gln Ile Pro Glu Val Leu Ile Ser Gly Asn Ala Gly Asp Val Val  
 835 840 845  
 Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu His Leu Pro His Thr Gly  
 850 855 860  
 Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr Ile Ser Gln Asn Thr Gly  
 865 870 875 880  
 Asn Val Leu Phe Tyr Asn Asn Val Ala Cys Ser Gly Gly Ala Val Arg  
 885 890 895  
 Ile Glu Asp His Gly Asn Val Leu Leu Glu Ala Phe Gly Gly Asp Ile  
 900 905 910  
 Val Phe Lys Gly Asn Ser Ser Phe Arg Ala Gln Gly Ser Asp Ala Ile  
 915 920 925  
 Tyr Phe Ala Gly Lys Glu Ser His Ile Thr Ala Leu Asn Ala Thr Glu  
 930 935 940  
 Gly His Ala Ile Val Phe His Asp Ala Leu Val Phe Glu Asn Leu Lys  
 945 950 955 960  
 Glu Arg Lys Ser Ala Glu Val Leu Leu Ile Asn Ser Arg Glu Asn Pro  
 965 970 975  
 Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu Ala Glu Ser Lys Val Pro  
 980 985 990  
 Gln Cys Ile His Val Gln Gln Gly Ser Leu Glu Leu Leu Asn Gly Ala  
 995 1000 1005  
 Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp Ala Gly Ala Lys Leu Val  
 1010 1015 1020  
 Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu Asp Ser Gly Thr Pro Val  
 1025 1030 1035 1040  
 Gln Gly His Ala Ile Ser Lys Pro Glu Ala Glu Ile Glu Ser Ser Ser

1045	1050	1055
Glu Pro Glu Gly Ala His Ser Leu Trp Ile Ala Lys Asn Ala Gln Thr		
1060	1065	1070
Thr Val Pro Met Val Asp Ile His Thr Ile Ser Val Asp Leu Ala Ser		
1075	1080	1085
Phe Ser Ser Ser Gln Gln Glu Gly Thr Val Glu Ala Pro Gln Val Ile		
1090	1095	1100
Val Pro Gly Gly Ser Tyr Val Arg Ser Gly Glu Leu Asn Leu Glu Leu		
1105	1110	1115
Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn His Ala Leu Leu Lys Asn		
1125	1130	1135
Glu Ala Lys Val Pro Leu Met Ser Phe Val Ala Ser Ser Asp Glu Ala		
1140	1145	1150
Ser Ala Glu Ile Ser Asn Leu Ser Val Ser Asp Leu Gln Ile His Val		
1155	1160	1165
Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr Gly His Met Gly Asp Trp		
1170	1175	1180
Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu Val Ile Asn Trp Asn Pro		
1185	1190	1195
Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala Gly Ala Leu Val Phe Asn		
1205	1210	1215
Ala Leu Trp Glu Glu Gly Ala Val Leu Ser Ala Leu Lys Asn Ala Arg		
1220	1225	1230
Phe Ala His Asn Leu Thr Ala Gln Arg Met Glu Phe Asp Tyr Ser Thr		
1235	1240	1245
Asn Val Trp Gly Phe Ala Phe Gly Gly Phe Arg Thr Leu Ser Ala Glu		
1250	1255	1260
Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly Ala Tyr Gly Gly Ala Ser		
1265	1270	1275
Ala Gly Val Asp Ile Gln Leu Met Glu Asp Phe Val Leu Gly Val Ser		
1285	1290	1295
Gly Ala Ala Phe Leu Gly Lys Met Asp Ser Gln Lys Phe Asp Ala Glu		
1300	1305	1310
Val Ser Arg Lys Gly Val Val Gly Ser Val Tyr Thr Gly Phe Leu Ala		
1315	1320	1325
Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser Leu Gly Glu Thr Gln Asn		
1330	1335	1340
Asp Met Lys Thr Arg Tyr Gly Val Leu Gly Glu Ser Ser Ala Ser Trp		
1345	1350	1355
Thr Ser Arg Gly Val Leu Ala Asp Ala Leu Val Glu Tyr Arg Ser Leu		
1365	1370	1375
Val Gly Pro Val Arg Pro Thr Phe Tyr Ala Leu His Phe Asn Pro Tyr		
1380	1385	1390
Val Glu Val Ser Tyr Ala Ser Met Lys Phe Pro Gly Phe Thr Glu Gln		
1395	1400	1405
Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala Ser Leu Thr Asn Ile Thr		
1410	1415	1420
Ile Pro Leu Gly Met Lys Phe Glu Leu Ala Phe Ile Lys Gly Gln Phe		
1425	1430	1435
Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr Ala Trp Glu Ala Tyr Arg		
1445	1450	1455
Lys Val Glu Gly Gly Ala Val Gln Leu Leu Glu Ala Gly Phe Asp Trp		
1460	1465	1470
Glu Gly Ala Pro Met Asp Leu Pro Arg Gln Glu Leu Arg Val Ala Leu		
1475	1480	1485

Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe Ser Thr Val Leu Gly Leu  
 1490 1495 1500  
 Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr Asp Ser Lys Leu Gly Tyr  
 1505 1510 1515 1520  
 Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe  
 1525 1530

<210> 179  
 <211> 1776  
 <212> PRT  
 <213> Chlamydia

<400> 179  
 Ala Ile Met Lys Phe Met Ser Ala Thr Ala Val Phe Ala Ala Val Leu  
 1 5 10 15  
 Ser Ser Val Thr Glu Ala Ser Ser Ile Gln Asp Gln Ile Lys Asn Thr  
 20 25 30  
 Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln Ala Phe Thr  
 35 40 45  
 Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala Asp Ser Val  
 50 55 60  
 Ser Phe Tyr Asp Phe Ser Thr Ser Gly Leu Pro Arg Lys His Leu  
 65 70 75 80  
 Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val Ser Ser Ser  
 85 90 95  
 Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala Pro Ser Ser  
 100 105 110  
 Gly Glu Thr Asp Lys Lys Thr Glu Glu Leu Asp Asn Gly Gly Ile  
 115 120 125  
 Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln Asp Ser Leu  
 130 135 140  
 Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe Gly Glu  
 145 150 155 160  
 Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn Gly Gly Ala  
 165 170 175  
 Ile Tyr Gly Glu Val Val Phe Glu Asn Ile Lys Ser Leu Leu  
 180 185 190  
 Val Glu Val Asn Ile Ser Val Glu Lys Gly Ser Val Tyr Ala Lys  
 195 200 205  
 Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe Ser Ser Asn  
 210 215 220  
 Gly Gly Glu Gln Gly Gly Ile Tyr Ser Glu Gln Asp Met Leu  
 225 230 235 240  
 Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala Ala Gly Ala  
 245 250 255  
 Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val Leu Thr  
 260 265 270  
 Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser Thr Pro Glu  
 275 280 285  
 Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser Ser Glu Thr  
 290 295 300  
 Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro Ser Pro Asp  
 305 310 315 320  
 Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys Ser Leu Thr  
 325 330 335

Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn Ile Ala Thr  
 340 345 350  
 Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser Cys Thr Asn  
 355 360 365  
 Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln His Gly Gly  
 370 375 380  
 Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr Thr Ser Glu  
 385 390 395 400  
 Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe Ser Glu Asn  
 405 410 415  
 Thr Ala Lys Gly His Gly Gly Ile Cys Thr Asn Lys Leu Ser Leu  
 420 425 430  
 Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala Lys Glu Ser  
 435 440 445  
 Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr Thr Asp Thr  
 450 455 460  
 Pro Glu Ser Ser Thr Pro Ser Ser Ser Pro Ala Ser Thr Pro Glu  
 465 470 475 480  
 Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser Thr Ala Glu  
 485 490 495  
 Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln Thr Asp Gln  
 500 505 510  
 Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser Ile Glu Asn  
 515 520 525  
 Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys Lys Gly Gly  
 530 535 540  
 Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn Asn Leu Glu  
 545 550 555 560  
 Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Gly Leu Cys Leu Thr  
 565 570 575  
 Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser His Tyr Asn  
 580 585 590  
 Ser Ala Ala Lys Glu Gly Gly Val Ile His Ser Lys Thr Val Thr Leu  
 595 600 605  
 Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr Val Lys Ala  
 610 615 620  
 Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro Pro Val Glu  
 625 630 635 640  
 Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn Thr Glu Gly  
 645 650 655  
 Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp Thr Ala Asp  
 660 665 670  
 Thr Gly Thr Gly Val Val Asn Asn Glu Ser Gln Asp Thr Ser Asp Thr  
 675 680 685  
 Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr Gln Ser Asn  
 690 695 700  
 Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser Asn Glu Asn  
 705 710 715 720  
 Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr Asp Glu Ser  
 725 730 735  
 Val Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln Asp Gly Gly  
 740 745 750  
 Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile Ser Ala Asn  
 755 760 765  
 Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser Ser Pro Val

770	775	780
Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp Asn Pro Asp		
785	790	795
Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly Pro Thr Glu		800
805	810	815
Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile Gly Gly Gly		
820	825	830
Ala Ile Tyr Gly Glu Thr Val Lys Ile Glu Asn Phe Ser Gly Gln Gly		
835	840	845
Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr Glu Gly Ser Ser		
850	855	860
Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala Lys Thr Leu Phe		880
865	870	875
Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr Phe Ser Gly Asn		
885	890	895
Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala Gly Gly Ala Ile		
900	905	910
Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val Phe Ser Lys Asn		
915	920	925
Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr Gln Arg Lys Asp		
930	935	940
Thr Phe Gly Gly Ala Ile Gly Ala Thr Ser Ala Val Ser Leu Ser Gly		960
945	950	955
Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly Ser Ala Ile Gly		
965	970	975
Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys Leu Glu Ser Gly		
980	985	990
Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg Ala Thr Ile Tyr		
995	1000	1005
Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr Phe Asn Gln Asn		
1010	1015	1020
Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr Lys Glu Ala Ser		
1025	1030	1035
Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn Leu Val Thr Pro		1040
1045	1050	1055
Thr Leu Ser Thr Thr Glu Gly Thr Pro Ala Thr Thr Ser Gly Asp		
1060	1065	1070
Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile Ala Ser Ser Asn		
1075	1080	1085
Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile Ala Ser Gly Gly		
1090	1095	1100
Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr Ser Ser Asp Thr		1120
1105	1110	1115
Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val Lys Leu Thr Met		
1125	1130	1135
Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp Ala Ile Arg Thr		
1140	1145	1150
Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr Asp Thr Leu Asp		
1155	1160	1165
Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser Ala Phe Thr Gly		
1170	1175	1180
Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro		
1185	1190	1195
Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu Lys Pro Asn Thr		1200
1205	1210	1215

Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly Ser Ser Leu Val  
 1220 1225 1230  
 Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val Ala Asp Gly Ala  
 1235 1240 1245  
 Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser Val Glu Lys Asn  
 1250 1255 1260  
 Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu Leu Arg Ile Ile  
 1265 1270 1275 1280  
 Asp Thr Thr Thr Ser Gly Ser Gly Thr Pro Ser Thr Asp Ser Glu  
 1285 1290 1295  
 Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn Asn Asn Asp Ala  
 1300 1305 1310  
 Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser Pro Ala Val Ala  
 1315 1320 1325  
 Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala Ala Ala Thr Ala  
 1330 1335 1340  
 Thr Pro Thr Thr Pro Thr Ala Thr Thr Thr Ser Asn Gln Val  
 1345 1350 1355 1360  
 Ile Leu Gly Glu Ile Lys Leu Ile Asp Pro Asn Gly Thr Phe Phe  
 1365 1370 1375  
 Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser Leu Leu Val Leu  
 1380 1385 1390  
 Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile Val Leu Thr Gly  
 1395 1400 1405  
 Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu Thr Leu Asp Pro  
 1410 1415 1420  
 Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp Lys Phe Asp Ser  
 1425 1430 1435 1440  
 Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His Phe Tyr Ala Asn  
 1445 1450 1455  
 Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val Lys Gln Gly Leu  
 1460 1465 1470  
 Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu Val Ser Tyr Asn  
 1475 1480 1485  
 Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser Gln Val Gly Thr  
 1490 1495 1500  
 Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly Ala Ser Val Ala  
 1505 1510 1515 1520  
 Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly Ala Ala Phe Ser  
 1525 1530 1535  
 Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu Asn Asn Tyr Thr  
 1540 1545 1550  
 His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val Tyr Gly Gly Lys  
 1555 1560 1565  
 Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys Ser Leu Pro Leu  
 1570 1575 1580  
 Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys His Asp Thr Val  
 1585 1590 1595 1600  
 Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly Glu Trp Glu Asp  
 1605 1610 1615  
 Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val Leu Arg Thr Pro  
 1620 1625 1630  
 Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly Glu Leu Glu Tyr  
 1635 1640 1645  
 Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu Tyr Asp Pro Arg

1650	1655	1660
Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile Pro Met Gly Leu		
1665	1670	1675
Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu Met Tyr Asn Arg		1680
1685	1690	1695
Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn Ser Pro Thr Cys		
1700	1705	1710
Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Gly Glu Ile Ile Cys Gly		
1715	1720	1725
Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser Thr Gln Leu Tyr		
1730	1735	1740
Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr Ile Glu Ala Asp		1760
1745	1750	1755
Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala Arg Met Thr Phe		
1765	1770	1775

&lt;210&gt; 180

&lt;211&gt; 1752

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

<400> 180	10	15
Met Lys Trp Leu Ser Ala Thr Ala Val Phe Ala Ala Val Leu Pro Ser		
1	5	
Val Ser Gly Phe Cys Phe Pro Glu Pro Lys Gln Leu Asn Phe Ser Arg		
20	25	30
Val Glu Thr Ser Ser Ser Thr Thr Phe Thr Glu Thr Ile Gly Glu Ala		
35	40	45
Gly Ala Glu Tyr Ile Val Ser Gly Asn Ala Ser Phe Thr Lys Phe Thr		
50	55	60
Asn Ile Pro Thr Thr Asp Thr Thr Pro Thr Asn Ser Asn Ser Ser		
65	70	75
Ser Ser Ser Gly Glu Thr Ala Ser Val Ser Glu Asp Ser Asp Ser Thr		80
85	90	95
Thr Thr Thr Pro Asp Pro Lys Gly Gly Ala Phe Tyr Asn Ala His		
100	105	110
Ser Gly Val Leu Ser Phe Met Thr Arg Ser Gly Thr Glu Gly Ser Leu		
115	120	125
Thr Leu Ser Glu Ile Lys Met Thr Gly Glu Gly Ala Ile Phe Ser		
130	135	140
Gln Gly Glu Leu Leu Phe Thr Asp Leu Thr Ser Leu Thr Ile Gln Asn		
145	150	155
Asn Leu Ser Gln Leu Ser Gly Gly Ala Ile Phe Gly Ser Thr Ile		160
165	170	175
Ser Leu Ser Gly Ile Thr Lys Ala Thr Phe Ser Cys Asn Ser Ala Glu		
180	185	190
Val Pro Ala Pro Val Lys Lys Pro Thr Glu Pro Lys Ala Gln Thr Ala		
195	200	205
Ser Glu Thr Ser Gly Ser Ser Ser Ser Gly Asn Asp Ser Val Ser		
210	215	220
Ser Pro Ser Ser Ser Arg Ala Glu Pro Ala Ala Asn Leu Gln Ser		
225	230	235
His Phe Ile Cys Ala Thr Ala Thr Pro Ala Ala Gln Thr Asp Thr Glu		240
245	250	255
Thr Ser Thr Pro Ser His Lys Pro Gly Ser Gly Gly Ala Ile Tyr Ala		

260	265	270
Lys Gly Asp Leu Thr Ile Ala Asp Ser Gln Glu Val Leu Phe Ser Ile		
275	280	285
Asn Lys Ala Thr Lys Asp Gly Gly Ala Ile Phe Ala Glu Lys Asp Val		
290	295	300
Ser Phe Glu Asn Ile Thr Ser Leu Lys Val Gln Thr Asn Gly Ala Glu		
305	310	315
Glu Lys Gly Gly Ala Ile Tyr Ala Lys Gly Asp Leu Ser Ile Gln Ser		
325	330	335
Ser Lys Gln Ser Leu Phe Asn Ser Asn Tyr Ser Lys Gln Gly Gly		
340	345	350
Ala Leu Tyr Val Glu Gly Gly Ile Asn Phe Gln Asp Leu Glu Glu Ile		
355	360	365
Arg Ile Lys Tyr Asn Lys Ala Gly Thr Phe Glu Thr Lys Lys Ile Thr		
370	375	380
Leu Pro Ser Leu Lys Ala Gln Ala Ser Ala Gly Asn Ala Asp Ala Trp		
385	390	395
Ala Ser Ser Ser Pro Gln Ser Gly Ser Gly Ala Thr Thr Val Ser Asp		
405	410	415
Ser Gly Asp Ser Ser Ser Gly Ser Asp Ser Asp Thr Ser Glu Thr Val		
420	425	430
Pro Val Thr Ala Lys Gly Gly Leu Tyr Thr Asp Lys Asn Leu Ser		
435	440	445
Ile Thr Asn Ile Thr Gly Ile Glu Ile Ala Asn Asn Lys Ala Thr		
450	455	460
Asp Val Gly Gly Gly Ala Tyr Val Lys Gly Thr Leu Thr Cys Glu Asn		
465	470	475
Ser His Arg Leu Gln Phe Leu Lys Asn Ser Ser Asp Lys Gln Gly Gly		
485	490	495
Gly Ile Tyr Gly Glu Asp Asn Ile Thr Leu Ser Asn Leu Thr Gly Lys		
500	505	510
Thr Leu Phe Gln Glu Asn Thr Ala Lys Glu Glu Gly Gly Leu Phe		
515	520	525
Ile Lys Gly Thr Asp Lys Ala Leu Thr Met Thr Gly Leu Asp Ser Phe		
530	535	540
Cys Leu Ile Asn Asn Thr Ser Glu Lys His Gly Gly Gly Ala Phe Val		
545	550	555
Thr Lys Glu Ile Ser Gln Thr Tyr Thr Ser Asp Val Glu Thr Ile Pro		
565	570	575
Gly Ile Thr Pro Val His Gly Glu Thr Val Ile Thr Gly Asn Lys Ser		
580	585	590
Thr Gly Gly Asn Gly Gly Val Cys Thr Lys Arg Leu Ala Leu Ser		
595	600	605
Asn Leu Gln Ser Ile Ser Ile Ser Gly Asn Ser Ala Ala Glu Asn Gly		
610	615	620
Gly Gly Ala His Thr Cys Pro Asp Ser Phe Pro Thr Ala Asp Thr Ala		
625	630	635
Glu Gln Pro Ala Ala Ala Ser Ala Ala Thr Ser Thr Pro Lys Ser Ala		
645	650	655
Pro Val Ser Thr Ala Leu Ser Thr Pro Ser Ser Ser Thr Val Ser Ser		
660	665	670
Leu Thr Leu Leu Ala Ala Ser Ser Gln Ala Ser Pro Ala Thr Ser Asn		
675	680	685
Lys Glu Thr Gln Asp Pro Asn Ala Asp Thr Asp Leu Leu Ile Asp Tyr		
690	695	700

Val Val Asp Thr Thr Ile Ser Lys Asn Thr Ala Lys Lys Gly Gly Gly  
 705 710 715 720  
 Ile Tyr Ala Lys Lys Ala Lys Met Ser Arg Ile Asp Gln Leu Asn Ile  
 725 730 735  
 Ser Glu Asn Ser Ala Thr Glu Ile Gly Gly Gly Ile Cys Cys Lys Glu  
 740 745 750  
 Ser Leu Glu Leu Asp Ala Leu Val Ser Leu Ser Val Thr Glu Asn Leu  
 755 760 765  
 Ser Thr Gly Val Ala Thr Thr Ala Ser Ala Pro Ala Ala Ala Ala  
 785 805 810 815  
 Ser Leu Gln Ala Ala Ala Ala Ala Pro Ser Ser Pro Ala Thr Pro  
 820 825 830  
 Thr Tyr Ser Gly Val Val Gly Gly Ala Ile Tyr Gly Glu Lys Val Thr  
 835 840 845  
 Phe Ser Gln Cys Ser Gly Thr Cys Gln Phe Ser Gly Asn Gln Ala Ile  
 850 855 860  
 Asp Asn Asn Pro Ser Gln Ser Ser Leu Asn Val Gln Gly Gly Ala Ile  
 865 870 875 880  
 Tyr Ala Lys Thr Ser Leu Ser Ile Gly Ser Ser Asp Ala Gly Thr Ser  
 885 890 895  
 Tyr Ile Phe Ser Gly Asn Ser Val Ser Thr Gly Lys Ser Gln Thr Thr  
 900 905 910  
 Gly Gln Ile Ala Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Leu Asn  
 915 920 925  
 Cys Pro Ala Thr Phe Ser Asn Asn Thr Ala Ser Ile Ala Thr Pro Lys  
 930 935 940  
 Thr Ser Ser Glu Asp Gly Ser Ser Gly Asn Ser Ile Lys Asp Thr Ile  
 945 950 955 960  
 Gly Gly Ala Ile Ala Gly Thr Ala Ile Thr Leu Ser Gly Val Ser Arg  
 965 970 975  
 Phe Ser Gly Asn Thr Ala Asp Leu Gly Ala Ala Ile Gly Thr Leu Ala  
 980 985 990  
 Asn Ala Asn Thr Pro Ser Ala Thr Ser Gly Ser Gln Asn Ser Ile Thr  
 995 1000 1005  
 Glu Lys Ile Thr Leu Glu Asn Gly Ser Phe Ile Phe Glu Arg Asn Gln  
 1010 1015 1020  
 Ala Asn Lys Arg Gly Ala Ile Tyr Ser Pro Ser Val Ser Ile Lys Gly  
 1025 1030 1035 1040  
 Asn Asn Ile Thr Phe Asn Gln Asn Thr Ser Thr His Asp Gly Ser Ala  
 1045 1050 1055  
 Ile Tyr Phe Thr Lys Asp Ala Thr Ile Glu Ser Leu Gly Ser Val Leu  
 1060 1065 1070  
 Phe Thr Gly Asn Asn Val Thr Ala Thr Gln Ala Ser Ser Ala Thr Ser  
 1075 1080 1085  
 Gly Gln Asn Thr Asn Thr Ala Asn Tyr Gly Ala Ala Ile Phe Gly Asp  
 1090 1095 1100  
 Pro Gly Thr Thr Gln Ser Ser Gln Thr Asp Ala Ile Leu Thr Leu Leu  
 1105 1110 1115 1120  
 Ala Ser Ser Gly Asn Ile Thr Phe Ser Asn Asn Ser Leu Gln Asn Asn  
 1125 1130 1135  
 Gln Gly Asp Thr Pro Ala Ser Lys Phe Cys Ser Ile Ala Gly Tyr Val

1140	1145	1150
Lys Leu Ser Leu Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp		
1155	1160	1165
Cys Val His Thr Ser Thr Lys Lys Thr Gly Ser Thr Gln Asn Val Tyr		
1170	1175	1180
Glu Thr Leu Asp Ile Asn Lys Glu Glu Asn Ser Asn Pro Tyr Thr Gly		
1185	1190	1195
Thr Ile Val Phe Ser Ser Glu Leu His Glu Asn Lys Ser Tyr Ile Pro		
1205	1210	1215
Gln Asn Ala Ile Leu His Asn Gly Thr Leu Val Leu Lys Glu Lys Thr		
1220	1225	1230
Glu Leu His Val Val Ser Phe Glu Gln Lys Glu Gly Ser Lys Leu Ile		
1235	1240	1245
Met Glu Pro Gly Ala Val Leu Ser Asn Gln Asn Ile Ala Asn Gly Ala		
1250	1255	1260
Leu Ala Ile Asn Gly Leu Thr Ile Asp Leu Ser Ser Met Gly Thr Pro		
1265	1270	1275
Gln Ala Gly Glu Ile Phe Ser Pro Pro Glu Leu Arg Ile Val Ala Thr		
1285	1290	1295
Thr Ser Ser Ala Ser Gly Gly Ser Gly Val Ser Ser Ser Ile Pro Thr		
1300	1305	1310
Asn Pro Lys Arg Ile Ser Ala Ala Val Pro Ser Gly Ser Ala Ala Thr		
1315	1320	1325
Thr Pro Thr Met Ser Glu Asn Lys Val Phe Leu Thr Gly Asp Leu Thr		
1330	1335	1340
Leu Ile Asp Pro Asn Gly Asn Phe Tyr Gln Asn Pro Met Leu Gly Ser		
1345	1350	1355
Asp Leu Asp Val Pro Leu Ile Lys Leu Pro Thr Asn Thr Ser Asp Val		
1365	1370	1375
Gln Val Tyr Asp Leu Thr Leu Ser Gly Asp Leu Phe Pro Gln Lys Gly		
1380	1385	1390
Tyr Met Gly Thr Trp Thr Leu Asp Ser Asn Pro Gln Thr Gly Lys Leu		
1395	1400	1405
Gln Ala Arg Trp Thr Phe Asp Thr Tyr Arg Arg Trp Val Tyr Ile Pro		
1410	1415	1420
Arg Asp Asn His Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Asn Ser		
1425	1430	1435
Met Ile Val Val Lys Gln Gly Leu Ile Asn Asn Met Leu Asn Asn Ala		
1445	1450	1455
Arg Phe Asp Asp Ile Ala Tyr Asn Asn Phe Trp Val Ser Gly Val Gly		
1460	1465	1470
Thr Phe Leu Ala Gln Gln Gly Thr Pro Leu Ser Glu Glu Phe Ser Tyr		
1475	1480	1485
Tyr Ser Arg Gly Thr Ser Val Ala Ile Asp Ala Lys Pro Arg Gln Asp		
1490	1495	1500
Phe Ile Leu Gly Ala Ala Phe Ser Lys Ile Val Gly Lys Thr Lys Ala		
1505	1510	1515
Ile Lys Lys Met His Asn Tyr Phe His Lys Gly Ser Glu Tyr Ser Tyr		
1525	1530	1535
Gln Ala Ser Val Tyr Gly Gly Lys Phe Leu Tyr Phe Leu Leu Asn Lys		
1540	1545	1550
Gln His Gly Trp Ala Leu Pro Phe Leu Ile Gln Gly Val Val Ser Tyr		
1555	1560	1565
Gly His Ile Lys His Asp Thr Thr Leu Tyr Pro Ser Ile His Glu		
1570	1575	1580

Arg Asn Lys Gly Asp Trp Glu Asp Leu Gly Trp Leu Ala Asp Leu Arg  
 1585 1590 1595 1600  
 Ile Ser Met Asp Leu Lys Glu Pro Ser Lys Asp Ser Ser Lys Arg Ile  
 1605 1610 1615  
 Thr Val Tyr Gly Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe  
 1620 1625 1630  
 Thr Glu Ile Asp Tyr Asp Pro Arg His Phe Asp Asp Cys Ala Tyr Arg  
 1635 1640 1645  
 Asn Leu Ser Leu Pro Val Gly Cys Ala Val Glu Gly Ala Ile Met Asn  
 1650 1655 1660  
 Cys Asn Ile Leu Met Tyr Asn Lys Leu Ala Leu Ala Tyr Met Pro Ser  
 1665 1670 1675 1680  
 Ile Tyr Arg Asn Asn Pro Val Cys Lys Tyr Arg Val Leu Ser Ser Asn  
 1685 1690 1695  
 Glu Ala Gly Gln Val Ile Cys Gly Val Pro Thr Arg Thr Ser Aia Arg  
 1700 1705 1710  
 Ala Glu Tyr Ser Thr Gln Leu Tyr Leu Gly Pro Phe Trp Thr Leu Tyr  
 1715 1720 1725  
 Gly Asn Tyr Thr Ile Asp Val Gly Met Tyr Thr Leu Ser Gln Met Thr  
 1730 1735 1740  
 Ser Cys Gly Aia Arg Met Ile Phe  
 1745 1750

&lt;210&gt; 181

&lt;211&gt; 2601

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

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agcctctttc ctgctctttg tgctcatgca tcacaagacg atcccttgta tgtaacttggaa	240
aattccactt gttggttcgt atctaaactc catatcacgg accccaaaaga ggctcttttt	300
aaagaaaaaaag gagatcttgc cattccaaac ttccgttccc ttcccttccac agattgtct	360
tccaaaggaaa gctctccccc tattattcat caaaaatgt gtcagttatc cttgcgcata	420
aatggtagca tgagttctg tcgaaatcat gctgaaggtt ctggaggagc catttctgcg	480
gatgcctttt ctctacagca caactatctt ttacacagctt ttgaagagaa ttcttctaaa	540
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atttggtgta tcagcgatct aaacacctca gaaaaaggct ctctctctct tgttgtAAC	780
caaraaaacgc tatttgcaag caattctgtc aaagaaaaag gccccgttat ttatgccaag	840
cacatggtat tgcgttataa cggccctgtt tccttcattt acaacacgc taaaataggt	900
ggagctatcg ccatccagtc cggaggaggat ctctctatcc ttgcagggtga agatctgtt	960
ctgttccaga ataactccca acgcacccctc gaccaagggtc tagtaagaaa cggccatctac	1020
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gatccattt gataagaaaaat tagcagaaaaaa gaatcgccctc ttccctccctc ttgcagcc	1140
agcgtgactt ctcccccccc acccaccgca tctccttttag ttattcagac aagtgcAAAC	1200
cgttcagtgta ttttctcgag cgaacgtctt tctgaagaaat aaaaaactcc tgataacctc	1260
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ttcctctcta actctggaga tgagaatttt tatgaaaaatg tagagctct cagtaaagag	1560
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ggaaacctct	tttctcaactt	tggatatacaa	ggagattgga	ctttttcttg	gaaagattct	1620
gatgaagggc	attctctgtat	tgctaattgg	acgcctaaaa	actatgtgcc	tcatccagaa	1680
cgtcaatcta	cactcggtgc	gaacacttctt	tgaacacac	attccgatat	gcaagctgtg	1740
cagtcatgtat	ttaatacacaac	agcgcacgga	ggagcctatc	tatggaaac	gtggggatct	1800
gctgtttctt	attttattctta	tgttcacgac	agctctggga	aacctatcga	taattggcat	1860
catagaagcc	ttggctaccc	attcggtatc	agtactcaca	gtttagatga	ccatttttc	1920
tgcttggctg	caggacaatt	actcgaaa	tgcgtccgatt	cctttattac	gtctacagaa	1980
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gcacaggcat	gctacaatga	aagtatccat	gagctaaaaa	caaaaatatcg	ctcctctct	2100
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cctattgtat	ccaatggttc	cggactgttc	agctccttct	ctattttctc	taaactgcaa	2220
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gccagcttt	ttagaaatat	ttagaaatata	ataggaataa	catttgaaaaa	aaaatccccaa	2340
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gaatcgggac	ctgttagtgtt	actcaaaaat	gccgtctct	gggatgtcc	tatggcgaac	2460
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gaatttactt attacagcg aggagcttct gttgcctttag atgctaaacc agcccatgat	2100
gtgatgttg gagctgttgcatt tagtaagatg atcggggaaaa caaaatcctt gaaaagagag	2160
aataactaca ctcacaaagg atccgaatata tcttaccaag catcgatata cggaggcaaa	2220
ccattccact ttgtatcaa taaaaaaacg gaaaatcgc taccgctatt gttacaaggaa	2280
gtcattctt acggatataat caaacatgtt acagtgttgc actatccaaac gatccgttgc	2340
cgaaaccaag gagaatgggaa agacttagga tggctgacag ctctccgtt ctcctctgtc	2400

ttaagaactc	ctgcacaagg	ggatactaaa	cgtatcactg	tttacggaga	atttgaatac	2460
tccagtatcc	gtcagaaaaca	attcacagaa	acagaatacg	atcctcgta	cttcgacaac	2520
tgcacctata	gaaacttagc	aattccatag	gggttagcat	tcgaaggaga	gctctctgg	2580
aacgatattt	tgatgtacaa	cagattctct	gtacgatatac	tgccatcaat	ctatcgaaat	2640
tctccaacat	gcaaatacc	agtgcctct	tcaggagaag	gcggagaaat	tatttgtgga	2700
gtacccacaa	gaaactcagc	tcgcggagaa	tacagcacgc	agctgtaccc	gggacctttg	2760
tggactctgt	atggatccta	cacgatagaa	gcagacgcac	atacactagc	tcatatgatg	2820
aactgcggtg	ctcgatgac	attctaa				2847

&lt;210&gt; 187

&lt;211&gt; 2466

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 187

atgcatcacc	atcaccatca	cgaggcgagc	tcgatccaag	atcaaataaa	gaataccgac	60
tgcaatgtta	gcaaagttag	atattaact	tctcaagcat	ttactgatat	gatgttagca	120
gacaacacag	agtatcgagc	tgcgtatagt	grttcattct	atgactttc	gacatcttcc	180
ggattaccta	gaaaacatct	tagtagtagt	agtgaagctt	ctccaaacgac	agaaggagtg	240
tcttcatctt	catctggaga	aaatactgag	aattcacaag	attcagctcc	ctttctggaa	300
gaaaactgata	agaaaacaga	agaagaacta	gacaatggcg	aatcattta	tgcgttagagag	360
aaactaacta	tctcagaatc	tcaggactct	ctctctaatt	caagcataga	actccatgac	420
aatagtttt	tcttcggaga	aggtgaagtt	atctttgatc	acagaggttgc	ctccaaaaac	480
ggggagct	tttatggaga	gaaagaggta	gtctttgaaa	acataaaatc	tctactagta	540
gaagtaata	tctcggtcga	gaaagggggt	agcgtctatg	caaaaagaacy	agtatcttta	600
gaaaatgtta	ccgaagcaac	cttctccctcc	aatgggtgggg	aacaagggtgg	tggtggaaatc	660
tattcagaac	aagatatgtt	aatcagtgtat	tgcaacaatg	tacatttcca	agggaatgct	720
gcaggagcaa	cagcagtaaa	acaatgtctg	gatgaagaaa	tgatcgatt	gctcacagaa	780
tgcgttata	gcttatccga	agatacactg	gatagcactc	cagaaacgga	acagactaag	840
tcaaatggaa	atcaagatgg	ttcgctctgaa	acaaaagata	cacaagtats	agatcacca	900
gaatcaactc	ctagccccga	cgatgtttt	gttaaagggtg	gtggtatctt	tacagaaaaaa	960
tcttgcacca	tcacttggaa	tacagggact	atagattttt	tcagtaacat	agctaccgat	1020
tctggagcag	gtgtatttac	taaagaaaac	ttgtcttgca	ccaacacgaa	tagctacag	1080
tttttggaaa	actcggcagg	tcaacatgga	ggaggagcc	acgttactca	aaccatgtct	1140
gttactaata	caacttagta	aagtataact	actccccctc	tcgttaggaga	agtattttc	1200
tctgaaaata	cagctaaagg	gcacgggtgt	gttatctgca	ctaacaaact	ttctttatct	1260
aattttaaaa	cggtgactct	caactaaaac	tctgcaaaagg	agtctggagg	agtattttt	1320
acagatctag	cgtctataacc	aacaacagat	accccagat	tttctacccc	ctttccctcc	1380
tcgcctgcaa	gcactcccg	agtagttgct	tctgtaaaaa	taatcgatt	cttgcctct	1440
acggcagaac	ccgcagcccc	ttctctaaaca	gaggctgagt	ctgatcaaac	ggatcaaaca	1500
gaaaactctg	atactaatag	cgatatagac	gtgtcgattt	agaacatttt	gaatgtcgct	1560
atcaatcaa	acacttctgc	aaaaaaaggaa	ggggcttattt	acggaaaaaa	agctaaactt	1620
tcccgattta	acaatcttga	actttcaggg	aattcatccc	aggatgttag	aggaggtctc	1680
tgtttaactg	aaagcgtaga	atttgcgtca	attggatcgc	tcttatccca	ctataactct	1740
gctgctaaag	aagggtgggt	tattcattct	aaaacggta	ctctatctaa	cctcaagtct	1800
accttcactt	ttgcagatata	cactgtttaa	gcaatagtag	aaagcactcc	tgaagctcca	1860
gaagagattc	ctcccgataga	aggagaagag	tctacagcaa	cagaaaaatcc	gaattctaat	1920
acagaaggaa	gttcggctaa	cactaacctt	gaaggatctc	aaggggatac	tgcgtataca	1980
gggactggtg	ttgttaccaa	tgagtctaa	gacacatctg	atactggaaa	cgcgtatct	2040
ggagaacaac	tacaagatcc	tacacaatct	aatgaagaaa	atacccttcc	caatagtagt	2100
attgatcaat	ctaacaaaaa	cacagacgaa	tcatctgata	gccacactga	ggaaataact	2160
gacgagatgt	tctcatcg	ctctaaaagt	ggatcatct	ctcctcaaga	tggaggagca	2220
gcttcttcag	gggctccctc	aggagatcaa	tctatctctg	caaacgcttg	tttagctaaa	2280
agctatctgt	cgagtaactga	tagtccccc	gtatctaatt	cttcagggttc	agacgttact	2340
gcatcttcgt	ataatccaga	ctctccctca	tctggagata	gcgctggaga	ctctgaagga	2400

ccgactgagc cagaagctgg ttctacaaca gaaactccta cttaatagg aggaggtgc	2460
atctga	2466

&lt;210&gt; 188

&lt;211&gt; 1578

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 188

atgcattcacc atcaccatca cacggcccg tccgataact tccagctgtc ccagggtggg	60
cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat caagctccc	120
accgttcata tcgggcctac cgccttctc ggcttgggtg ttgtcgacaa caacggcaac	180
ggcgcacgag tccaacgcgt ggtcgggagc gctccggcgg caagtctcg catctccacc	240
ggcgcacgtga tcaaccgcgt cgacggcgct ccatcaact cggccaccgc gatggcggac	300
gcgcctaacc ggcattcatcc cggtgacgatc atctcggtga cttggcaaac caagtccggc	360
ggcacgcgtt cagggAACgt gacattggcc gagggacccc cggccgaatt ccccttagta	420
cctagagggtt caccgcgtcc tggggaaat ccagctgaac caagtttatt aatcgatggc	480
actatgtggg aagggtgcgtt agaggatct tgcgatcctt gcgcacttgc gtgtgacgcc	540
attagcatcc ggcgcaggata ctacggagat tatgttttcg atcggttatt aaaagttgat	600
gtgaataaaa ctttttagcgg catggctgca actcctacgc aggctataagg taacgcaagt	660
aatactaatac agccagaagg aaatggcaga cccaaacatcg cttacggaaag gcatatgca	720
gatgcagagt gttttcaaa tgcagccttc ctagccttaa acatttggga tgcgttcgac	780
atttctgca ctttaggggc atccaatggta tacttcaaag caagttccgc tgcattcaac	840
ttgggtgggt taatagggtt ttcagctgca agctcaatct ctaccgatct tccaaatgca	900
cttcctaacc taggcattac ccaagggttt gtggatattt atacagacac atcatttct	960
tggagcgttag gtgcacgtgg agcttatgg gaatgtgggt gtgcacccaggagctgag	1020
ttccaaatcgt ctcatactaa tccataagatt gagatgctca acgtcacttc aagcccgca	1080
caatttgtga ttcacaaaacc aagaggctat aaaggagcta gctcaattt tccttacct	1140
ataacggctg gaacaacaga agctacagac accaaatcag ctacaatcaa ataccatgaa	1200
tggcaagtag gcctcgcccc gtcttacaga ttgaatatgc ttgttccata tattggcgt	1260
aactggctaa gagcaactt tgatgctgat actatccgca ttgctcaacc taaattaaaa	1320
tcggagattt ttaacattac tacatggaaac ccaaggctta taggatcaac cactgcttt	1380
cccaataataa gtggtaagga tggctatct gatgtttgc aaattgcttc gattcagatc	1440
aacaaaatga agtctagaaa agcttggtt gtagctgttgc gtgcacgtt aatcgacgt	1500
gacaaatggt caatcactgg tgaagcacgc ttaatcaatg aaagagctgc tcacatgaat	1560
gcacaattcc gcttctaa	1578

&lt;210&gt; 189

&lt;211&gt; 866

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(866)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 189

Met Ala Ser His His His His His Leu Phe Gly Gln Asp Pro Leu	
1 5 10 15	
Gly Glu Thr Ala Leu Leu Thr Lys Asn Pro Asn His Val Val Cys Thr	
20 25 30	
Phe Phe Glu Asp Cys Thr Met Glu Ser Leu Phe Pro Ala Leu Cys Ala	
35 40 45	
His Ala Ser Gln Asp Asp Pro Leu Tyr Val Leu Gly Asn Ser Tyr Cys	

50	55	60
Trp Phe Val Ser Lys Leu His Ile Thr Asp Pro Lys Glu Ala Leu Phe		
	70	75
Lys Glu Lys Gly Asp Leu Ser Ile Gln Asn Phe Arg Phe Leu Ser Phe		80
	85	90
Thr Asp Cys Ser Ser Lys Glu Ser Ser Pro Ser Ile Ile His Gln Lys		95
	100	105
Asn Gly Gln Leu Ser Leu Arg Asn Asn Gly Ser Met Ser Phe Cys Arg		110
	115	120
Asn His Ala Glu Gly Ser Gly Gly Ala Ile Ser Ala Asp Ala Phe Ser		125
	130	135
Leu Gln His Asn Tyr Leu Phe Thr Ala Phe Glu Glu Asn Ser Ser Lys		140
	145	150
Gly Asn Gly Gly Ala Ile Gln Ala Gln Thr Phe Ser Leu Ser Arg Asn		160
	165	170
Val Ser Pro Ile Ser Phe Ala Arg Asn Arg Ala Asp Leu Asn Gly Gly		175
	180	185
Ala Ile Cys Cys Ser Asn Leu Ile Cys Ser Gly Asn Val Asn Pro Leu		190
	195	200
Phe Phe Thr Gly Asn Ser Ala Thr Asn Gly Gly Xaa Ile Cys Cys Ile		205
	210	215
Ser Asp Leu Asn Thr Ser Glu Lys Gly Ser Leu Ser Leu Ala Cys Asn		220
	225	230
Gln Xaa Thr Leu Phe Ala Ser Asn Ser Ala Lys Glu Lys Gly Gly Ala		240
	245	250
Ile Tyr Ala Lys His Met Val Leu Arg Tyr Asn Gly Pro Val Ser Phe		255
	260	265
Ile Asn Asn Ser Ala Lys Ile Gly Gly Ala Ile Ala Ile Gln Ser Gly		270
	275	280
Gly Ser Leu Ser Ile Leu Ala Gly Glu Gly Ser Val Leu Phe Gln Asn		285
	290	295
Asn Ser Gln Arg Thr Ser Asp Gln Gly Leu Val Arg Asn Ala Ile Tyr		300
	305	310
Leu Glu Lys Asp Ala Ile Leu Ser Ser Leu Glu Ala Arg Asn Gly Asp		320
	325	330
Ile Leu Phe Phe Asp Pro Ile Val Gln Glu Ser Ser Lys Glu Ser		335
	340	345
Pro Leu Pro Ser Ser Leu Gln Ala Ser Val Thr Ser Pro Thr Pro Ala		350
	355	360
Thr Ala Ser Pro Leu Val Ile Gln Thr Ser Ala Asn Arg Ser Val Ile		365
	370	375
Phe Ser Ser Glu Arg Leu Ser Glu Glu Lys Thr Pro Asp Asn Leu		380
	385	390
Thr Ser Gln Leu Gln Gln Pro Ile Glu Leu Lys Ser Gly Arg Leu Val		395
	405	410
Leu Lys Asp Arg Ala Val Leu Ser Xaa Pro Ser Leu Ser Gln Asp Pro		400
	420	425
Gln Ala Leu Leu Ile Met Glu Ala Gly Thr Ser Leu Lys Thr Ser Xaa		415
	435	440
Asp Leu Lys Leu Xaa Thr Xaa Ser Ile Pro Leu His Ser Leu Asp Thr		430
	450	455
Glu Lys Ser Val Thr Ile His Ala Pro Asn Leu Ser Ile Gln Lys Ile		445
	465	470
Phe Leu Ser Asn Ser Gly Asp Glu Asn Phe Tyr Glu Asn Val Glu Leu		480
	485	490
		495

Leu Ser Lys Glu Gln Asn Asn Ile Pro Leu Leu Thr Leu Pro Lys Glu  
                   500                  505                  510  
 Gln Ser His Leu His Leu Pro Asp Gly Asn Leu Ser Ser His Phe Gly  
                   515                  520                  525  
 Tyr Gln Gly Asp Trp Thr Phe Ser Trp Lys Asp Ser Asp Glu Gly His  
                   530                  535                  540  
 Ser Leu Ile Ala Asn Trp Thr Pro Lys Asn Tyr Val Pro His Pro Glu  
                   545                  550                  555                  560  
 Arg Gln Ser Thr Leu Val Ala Asn Thr Leu Trp Asn Thr Tyr Ser Asp  
                   565                  570                  575  
 Met Gln Ala Val Gln Ser Met Ile Asn Thr Thr Ala His Gly Gly Ala  
                   580                  585                  590  
 Tyr Leu Phe Gly Thr Trp Gly Ser Ala Val Ser Asn Leu Phe Tyr Val  
                   595                  600                  605  
 His Asp Ser Ser Gly Lys Pro Ile Asp Asn Trp His His Arg Ser Leu  
                   610                  615                  620  
 Gly Tyr Leu Phe Gly Ile Ser Thr His Ser Leu Asp Asp His Ser Phe  
                   625                  630                  635                  640  
 Cys Leu Ala Ala Gly Gln Leu Leu Gly Lys Ser Ser Asp Ser Phe Ile  
                   645                  650                  655  
 Thr Ser Thr Glu Thr Thr Ser Tyr Ile Ala Thr Val Gln Ala Gln Leu  
                   660                  665                  670  
 Ala Thr Ser Leu Met Lys Ile Ser Ala Gln Ala Cys Tyr Asn Glu Ser  
                   675                  680                  685  
 Ile His Glu Leu Lys Thr Lys Tyr Arg Ser Phe Ser Lys Glu Gly Phe  
                   690                  695                  700  
 Gly Ser Trp His Ser Val Ala Val Ser Gly Glu Val Cys Ala Ser Ile  
                   705                  710                  715                  720  
 Pro Ile Val Ser Asn Gly Ser Gly Leu Phe Ser Ser Phe Ser Ile Phe  
                   725                  730                  735  
 Ser Lys Leu Gln Gly Phe Ser Gly Thr Gln Asp Gly Phe Glu Glu Ser  
                   740                  745                  750  
 Ser Gly Glu Ile Arg Ser Phe Ser Ala Ser Ser Phe Arg Asn Ile Ser  
                   755                  760                  765  
 Leu Pro Ile Gly Ile Thr Phe Glu Lys Lys Ser Gln Lys Thr Arg Thr  
                   770                  775                  780  
 Tyr Tyr Tyr Phe Leu Gly Ala Tyr Ile Gln Asp Leu Lys Arg Asp Val  
                   785                  790                  795                  800  
 Glu Ser Gly Pro Val Val Leu Leu Lys Asn Ala Val Ser Trp Asp Ala  
                   805                  810                  815  
 Pro Met Ala Asn Leu Asp Ser Arg Ala Tyr Met Phe Arg Leu Thr Asn  
                   820                  825                  830  
 Gln Arg Ala Leu His Arg Leu Gln Thr Leu Leu Asn Val Ser Cys Val  
                   835                  840                  845  
 Leu Arg Gly Gln Ser His Ser Tyr Ser Leu Asp Leu Gly Thr Thr Tyr  
                   850                  855                  860  
 Arg Phe  
                   865

&lt;210&gt; 190

&lt;211&gt; 1006

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;400&gt; 190

Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu  
 1 5 10 15  
 Val Pro His His His His His Met Ile Pro Gln Gly Ile Tyr Asp  
 20 25 30  
 Gly Glu Thr Leu Thr Val Ser Phe Pro Tyr Thr Val Ile Gly Asp Pro  
 35 40 45  
 Ser Gly Thr Thr Val Phe Ser Ala Gly Glu Leu Thr Leu Lys Asn Leu  
 50 55 60  
 Asp Asn Ser Ile Ala Ala Leu Pro Leu Ser Cys Phe Gly Asn Leu Leu  
 65 70 75 80  
 Gly Ser Phe Thr Val Leu Gly Arg Gly His Ser Leu Thr Phe Glu Asn  
 85 90 95  
 Ile Arg Thr Ser Thr Asn Gly Ala Ala Leu Ser Asn Ser Ala Ala Asp  
 100 105 110  
 Gly Leu Phe Thr Ile Glu Gly Phe Lys Glu Leu Ser Phe Ser Asn Cys  
 115 120 125  
 Asn Ser Leu Leu Ala Val Leu Pro Ala Ala Thr Thr Asn Lys Gly Ser  
 130 135 140  
 Asn Leu Val Ser Gly Asp Gly Ala Ile Asp Ala Lys Ser Leu Thr  
 180 185 190  
 Val Gln Gly Ile Ser Lys Leu Cys Val Phe Gln Glu Asn Thr Ala Gln  
 195 200 205  
 Ala Asp Gly Gly Ala Cys Gln Val Val Thr Ser Phe Ser Ala Met Ala  
 210 215 220  
 Asn Glu Ala Pro Ile Ala Phe Val Ala Asn Val Ala Gly Val Arg Gly  
 225 230 235 240  
 Gly Gly Ile Ala Ala Val Gln Asp Gly Gln Gln Gly Val Ser Ser Ser  
 245 250 255  
 Thr Ser Thr Glu Asp Pro Val Val Ser Phe Ser Arg Asn Thr Ala Val  
 260 265 270  
 Glu Phe Asp Gly Asn Val Ala Arg Val Gly Gly Ile Tyr Ser Tyr  
 275 280 285  
 Gly Asn Val Ala Phe Leu Asn Asn Gly Lys Thr Leu Phe Leu Asn Asn  
 290 295 300  
 Val Ala Ser Pro Val Tyr Ile Ala Ala Lys Gln Pro Thr Ser Gly Gln  
 305 310 315 320  
 Ala Ser Asn Thr Ser Asn Asn Tyr Gly Asp Gly Gly Ala Ile Phe Cys  
 325 330 335  
 Lys Asn Gly Ala Gln Ala Gly Ser Asn Asn Ser Gly Ser Val Ser Phe  
 340 345 350  
 Asp Gly Glu Gly Val Val Phe Phe Ser Ser Asn Val Ala Ala Gly Lys  
 355 360 365  
 Gly Gly Ala Ile Tyr Ala Lys Lys Leu Ser Val Ala Asn Cys Gly Pro  
 370 375 380  
 Val Gln Phe Leu Arg Asn Ile Ala Asn Asp Gly Gly Ala Ile Tyr Leu  
 385 390 395 400  
 Gly Glu Ser Gly Glu Leu Ser Leu Ser Ala Asp Tyr Gly Asp Ile Ile  
 405 410 415  
 Phe Asp Gly Asn Leu Lys Arg Thr Ala Lys Glu Asn Ala Ala Asp Val  
 420 425 430  
 Asn Gly Val Thr Val Ser Ser Gln Ala Ile Ser Met Gly Ser Gly Gly

435	440	445
Lys Ile Thr Thr Leu Arg Ala	Lys Ala Gly His Gln Ile Leu Phe Asn	
450	455	460
Asp Pro Ile Glu Met Ala Asn Gly Asn Asn Gln Pro Ala Gln Ser Ser		
465	470	475
Lys Leu Leu Lys Ile Asn Asp Gly Glu Gly Tyr Thr Gly Asp Ile Val		480
485	490	495
Phe Ala Asn Gly Ser Ser Thr Leu Tyr Gln Asn Val Thr Ile Glu Gln		
500	505	510
Gly Arg Ile Val Leu Arg Glu Lys Ala Lys Leu Ser Val Asn Ser Leu		
515	520	525
Ser Gln Thr Gly Gly Ser Leu Tyr Met Glu Ala Gly Ser Thr Leu Asp		
530	535	540
Phe Val Thr Pro Gln Pro Pro Gln Gln Prc Pro Ala Ala Asn Gln Leu		
545	550	555
Ile Thr Leu Ser Asn Leu His Leu Ser Leu Ser Ser Leu Leu Ala Asn		560
565	570	575
Asn Ala Val Thr Asn Pro Pro Thr Asn Pro Pro Ala Gln Asp Ser His		
580	585	590
Pro Ala Val Ile Gly Ser Thr Thr Ala Gly Ser Val Thr Ile Ser Gly		
595	600	605
Pro Ile Phe Phe Glu Asp Leu Asp Asp Thr Ala Tyr Asp Arg Tyr Asp		
610	615	620
Trp Leu Gly Ser Asn Gln Lys Ile Asn Val Leu Lys Leu Gln Leu Gly		
625	630	635
Thr Lys Pro Pro Ala Asn Ala Pro Ser Asp Leu Thr Leu Gly Asn Glu		640
645	650	655
Met Pro Lys Tyr Gly Tyr Gln Gly Ser Trp Lys Leu Ala Trp Asp Pro		
660	665	670
Asn Thr Ala Asn Asn Gly Pro Tyr Thr Leu Lys Ala Thr Trp Thr Lys		
675	680	685
Thr Gly Tyr Asn Pro Gly Pro Glu Arg Val Ala Ser Leu Val Pro Asn		
690	695	700
Ser Leu Trp Gly Ser Ile Leu Asp Ile Arg Ser Ala His Ser Ala Ile		
705	710	715
Gln Ala Ser Val Asp Gly Arg Ser Tyr Cys Arg Gly Leu Trp Val Ser		720
725	730	735
Gly Val Ser Asn Phe Phe Tyr His Asp Arg Asp Ala Leu Gly Gln Gly		
740	745	750
Tyr Arg Tyr Ile Ser Gly Gly Tyr Ser Leu Gly Ala Asn Ser Tyr Phe		
755	760	765
Gly Ser Ser Met Phe Gly Leu Ala Phe Thr Glu Val Phe Gly Arg Ser		
770	775	780
Lys Asp Tyr Val Val Cys Arg Ser Asn His His Ala Cys Ile Gly Ser		
785	790	795
Val Tyr Leu Ser Thr Gln Gln Ala Leu Cys Gly Ser Tyr Leu Phe Gly		800
805	810	815
Asp Ala Phe Ile Arg Ala Ser Tyr Gly Phe Gly Asn Gln His Met Lys		
820	825	830
Thr Ser Tyr Thr Phe Ala Glu Glu Ser Asp Val Arg Trp Asp Asn Asn		
835	840	845
Cys Leu Ala Gly Glu Ile Gly Ala Gly Leu Pro Ile Val Ile Thr Pro		
850	855	860
Ser Lys Leu Tyr Leu Asn Glu Leu Arg Pro Phe Val Gln Ala Glu Phe		
865	870	880

Ser	Tyr	Ala	Asp	His	Glu	Ser	Phe	Thr	Glu	Glu	Gly	Asp	Gln	Ala	Arg
									885	890				895	
Ala	Phe	Lys	Ser	Gly	His	Leu	Leu	Asn	Leu	Ser	Val	Pro	Val	Gly	Val
									900	905				910	
Lys	Phe	Asp	Arg	Cys	Ser	Ser	Thr	His	Pro	Asn	Lys	Tyr	Ser	Phe	Met
								915	920			925			
Ala	Ala	Tyr	Ile	Cys	Asp	Ala	Tyr	Arg	Thr	Ile	Ser	Gly	Thr	Glu	Thr
									930	935		940			
Thr	Leu	Leu	Ser	His	Gln	Glu	Thr	Trp	Thr	Asp	Ala	Phe	His	Leu	
								945	950		955			960	
Ala	Arg	His	Gly	Val	Val	Val	Arg	Gly	Ser	Met	Tyr	Ala	Ser	Leu	Thr
								965	970				975		
Ser	Asn	Ile	Glu	Val	Tyr	Gly	His	Gly	Arg	Tyr	Glu	Tyr	Arg	Asp	Ala
									980	985		990			
Ser	Arg	Gly	Tyr	Gly	Leu	Ser	Ala	Gly	Ser	Lys	Val	Arg	Phe		
									995	1000		1005			

<210> 191  
<211> 977  
<212> PRT  
<213> Chlamydia

<400> 191  
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu  
 1 5 10 15  
 Val Pro Ser Ser Asp Pro His His His His His His Gly Leu Ala Arg  
 20 25 30  
 Glu Val Pro Ser Arg Ile Phe Leu Met Pro Asn Ser Val Pro Asp Pro  
 35 40 45  
 Thr Lys Glu Ser Leu Ser Asn Lys Ile Ser Leu Thr Gly Asp Thr His  
 50 55 60  
 Asn Leu Thr Asn Cys Tyr Leu Asp Asn Leu Arg Tyr Ile Leu Ala Ile  
 65 70 75 80  
 Leu Gln Lys Thr Pro Asn Glu Gly Ala Ala Val Thr Ile Thr Asp Tyr  
 85 90 95  
 Leu Ser Phe Phe Asp Thr Gln Lys Glu Gly Ile Tyr Phe Ala Lys Asn  
 100 105 110  
 Leu Thr Pro Glu Ser Gly Gly Ala Ile Gly Tyr Ala Ser Pro Asn Ser  
 115 120 125  
 Pro Thr Val Glu Ile Arg Asp Thr Ile Gly Pro Val Ile Phe Glu Asn  
 130 135 140  
 Asn Thr Cys Cys Arg Leu Phe Thr Trp Arg Asn Pro Tyr Ala Ala Asp  
 145 150 155 160  
 Lys Ile Arg Glu Gly Gly Ala Ile His Ala Gln Asn Leu Tyr Ile Asn  
 165 170 175  
 His Asn His Asp Val Val Gly Phe Met Lys Asn Phe Ser Tyr Val Gln  
 180 185 190  
 Gly Gly Ala Ile Ser Thr Ala Asn Thr Phe Val Val Ser Glu Asn Gln  
 195 200 205  
 Ser Cys Phe Leu Phe Met Asp Asn Ile Cys Ile Gln Thr Asn Thr Ala  
 210 215 220  
 Gly Lys Gly Gly Ala Ile Tyr Ala Gly Thr Ser Asn Ser Phe Glu Ser  
 225 230 235 240  
 Asn Asn Cys Asp Leu Phe Phe Ile Asn Asn Ala Cys Cys Ala Gly Gly  
 245 250 255

Ala Ile Phe Ser Pro Ile Cys Ser Leu Thr Gly Asn Arg Gly Asn Ile  
           260                  265                  270  
 Val Phe Tyr Asn Asn Arg Cys Phe Lys Asn Val Glu Thr Ala Ser Ser  
           275                  280                  285  
 Glu Ala Ser Asp Gly Gly Ala Ile Lys Val Thr Thr Arg Leu Asp Val  
           290                  295                  300  
 Thr Gly Asn Arg Gly Arg Ile Phe Phe Ser Asp Asn Ile Thr Lys Asn  
           305                  310                  315                  320  
 Tyr Gly Gly Ala Ile Tyr Ala Pro Val Val Thr Leu Val Asp Asn Gly  
           325                  330                  335  
 Pro Thr Tyr Phe Ile Asn Asn Ile Ala Asn Asn Lys Gly Gly Ala Ile  
           340                  345                  350  
 Tyr Ile Asp Gly Thr Ser Asn Ser Lys Ile Ser Ala Asp Arg His Ala  
           355                  360                  365  
 Ile Ile Phe Asn Glu Asn Ile Val Thr Asn Val Thr Asn Ala Asn Gly  
           370                  375                  380  
 Thr Ser Thr Ser Ala Asn Pro Pro Arg Arg Asn Ala Ile Thr Val Ala  
           385                  390                  395                  400  
 Ser Ser Ser Gly Glu Ile Leu Leu Gly Ala Gly Ser Ser Gln Asn Leu  
           405                  410                  415  
 Ile Phe Tyr Asp Pro Ile Glu Val Ser Asn Ala Gly Val Ser Val Ser  
           420                  425                  430  
 Phe Asn Lys Glu Ala Asp Gln Thr Gly Ser Val Val Phe Ser Gly Ala  
           435                  440                  445  
 Thr Val Asn Ser Ala Asp Phe His Gln Arg Asn Leu Gln Thr Lys Thr  
           450                  455                  460  
 Pro Ala Pro Leu Thr Leu Ser Asn Gly Phe Leu Cys Ile Glu Asp His  
           465                  470                  475                  480  
 Ala Gln Leu Thr Val Asn Arg Phe Thr Gln Thr Gly Gly Val Val Ser  
           485                  490                  495  
 Leu Gly Asn Gly Ala Val Leu Ser Cys Tyr Lys Asn Gly Thr Gly Asp  
           500                  505                  510  
 Ser Ala Ser Asn Ala Ser Ile Thr Leu Lys His Ile Gly Leu Asn Leu  
           515                  520                  525  
 Ser Ser Ile Leu Lys Ser Gly Ala Glu Ile Pro Leu Leu Trp Val Glu  
           530                  535                  540  
 Pro Thr Asn Asn Ser Asn Asn Tyr Thr Ala Asp Thr Ala Ala Thr Phe  
           545                  550                  555                  560  
 Ser Leu Ser Asp Val Lys Leu Ser Leu Ile Asp Asp Tyr Gly Asn Ser  
           565                  570                  575  
 Pro Tyr Glu Ser Thr Asp Leu Thr His Ala Leu Ser Ser Gln Pro Met  
           580                  585                  590  
 Leu Ser Ile Ser Glu Ala Ser Asp Asn Gln Leu Gln Ser Glu Asn Ile  
           595                  600                  605  
 Asp Phe Ser Gly Leu Asn Val Pro His Tyr Gly Trp Gln Gly Leu Trp  
           610                  615                  620  
 Thr Trp Gly Trp Ala Lys Thr Gln Asp Pro Glu Pro Ala Ser Ser Ala  
           625                  630                  635                  640  
 Thr Ile Thr Asp Pro Gln Lys Ala Asn Arg Phe His Arg Thr Leu Leu  
           645                  650                  655  
 Leu Thr Trp Leu Pro Ala Gly Tyr Val Pro Ser Pro Lys His Arg Ser  
           660                  665                  670  
 Pro Leu Ile Ala Asn Thr Leu Trp Gly Asn Met Leu Leu Ala Thr Glu  
           675                  680                  685  
 Ser Leu Lys Asn Ser Ala Glu Leu Thr Pro Ser Gly His Pro Phe Trp

690	695	700
Gly Ile Thr Gly Gly	Leu Gly Met Met	Val Tyr Gln Asp Pro Arg
	710	720
705 Glu Asn His Pro Gly	Phe His Met Arg Ser Ser	Gly Tyr Ser Ala Gly
	725	735
Met Ile Ala Gly Gln Thr His	Thr Phe Ser Leu Lys	Phe Ser Gln Thr
	740	750
Tyr Thr Lys Leu Asn Glu Arg	Tyr Ala Lys Asn Asn Val	Ser Ser Lys
	755	765
Asn Tyr Ser Cys Gln Gly	Glu Met Leu Phe Ser	Leu Gln Glu Gly Phe
	770	780
Leu Leu Thr Lys Leu Val	Gly Leu Tyr Ser	Tyr Gly Asp His Asn Cys
	790	800
785 His His Phe Tyr Thr Gln	Gly Glu Asn Leu Thr	Ser Gln Gly Thr Phe
	805	815
Arg Ser Gln Thr Met Gly	Gly Ala Val Phe Phe	Asp Leu Pro Met Lys
	820	830
Pro Phe Gly Ser Thr His	Ile Leu Thr Ala Pro Phe	Leu Gly Ala Leu
	835	845
Gly Ile Tyr Ser Ser Leu	Ser His Phe Thr Glu Val	Gly Ala Tyr Pro
	850	860
Arg Ser Phe Ser Thr Lys	Thr Pro Leu Ile Asn Val	Leu Val Pro Ile
	865	880
Gly Val Lys Gly Ser Phe	Met Asn Ala Thr His	Arg Pro Gln Ala Trp
	885	895
Thr Val Glu Leu Ala Tyr	Gln Pro Val Leu Tyr	Arg Gln Glu Pro Gly
	900	910
Ile Ala Thr Gln Leu Leu	Ala Ser Lys Gly Ile Trp	Phe Gly Ser Gly
	915	925
Ser Pro Ser Ser Arg His	Ala Met Ser Tyr Lys	Ile Ser Gln Gln Thr
	930	940
Gln Pro Leu Ser Trp	Leu Thr Leu His Phe	Gln Tyr His Gly Phe Tyr
	945	960
Ser Ser Ser Thr Phe Cys	Asn Tyr Leu Asn Gly	Glu Ile Ala Leu Arg
	965	975
Phe		

<210> 192  
<211> 848  
<212> PRT  
<213> Chlamydia

<400> 192				
Met Ala Ser His His His His	Gly Ala Ile Ser Cys Leu Arg			
	10	15		
1	5			
Gly Asp Val Val Ile Ser Gly	Asn Lys Gly Arg Val Glu Phe Lys Asp			
	20	25	30	
Asn Ile Ala Thr Arg Leu Tyr	Val Glu Glu Thr Val Glu Lys Val Glu			
	35	40	45	
Glu Val Glu Pro Ala Pro	Glu Gln Lys Asp Asn Asn Glu Leu Ser Phe			
	50	55	60	
Leu Gly Ser Val Glu Gln	Ser Phe Ile Thr Ala Ala Asn Gln Ala Leu			
	65	70	75	80
Phe Ala Ser Glu Asp	Gly Asp Leu Ser Pro Glu Ser Ser Ile Ser Ser			

85	90	95
Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala Gly Gly Ala Ile Phe Ala		
100	105	110
Lys Arg Val Arg Ile Val Asp Asn Gln Glu Ala Val Val Phe Ser Asn		
115	120	125
Asn Phe Ser Asp Ile Tyr Gly Gly Ala Ile Phe Thr Gly Ser Leu Arg		
130	135	140
Glu Glu Asp Lys Leu Asp Gly Gln Ile Pro Glu Val Leu Ile Ser Gly		
145	150	155
Asn Ala Gly Asp Val Val Phe Ser Gly Asn Ser Ser Lys Arg Asp Glu		
165	170	175
His Leu Pro His Thr Gly Gly Ala Ile Cys Thr Gln Asn Leu Thr		
180	185	190
Ile Ser Gln Asn Thr Gly Asn Val Leu Phe Tyr Asn Asn Val Ala Cys		
195	200	205
Ser Gly Gly Ala Val Arg Ile Glu Asp His Gly Asn Val Leu Leu Glu		
210	215	220
Ala Phe Gly Gly Asp Ile Val Phe Lys Gly Asn Ser Ser Phe Arg Ala		
225	230	235
Gln Gly Ser Asp Ala Ile Tyr Phe Ala Gly Lys Glu Ser His Ile Thr		
245	250	255
Ala Leu Asn Ala Thr Glu Gly His Ala Ile Val Phe His Asp Ala Leu		
260	265	270
Val Phe Glu Asn Leu Lys Glu Arg Lys Ser Ala Glu Val Leu Leu Ile		
275	280	285
Asn Ser Arg Glu Asn Pro Gly Tyr Thr Gly Ser Ile Arg Phe Leu Glu		
290	295	300
Ala Glu Ser Lys Val Pro Gln Cys Ile His Val Gln Gln Gly Ser Leu		
305	310	315
Glu Leu Leu Asn Gly Ala Thr Leu Cys Ser Tyr Gly Phe Lys Gln Asp		
325	330	335
Ala Gly Ala Lys Leu Val Leu Ala Ala Gly Ser Lys Leu Lys Ile Leu		
340	345	350
Asp Ser Gly Thr Pro Val Gln Gly His Ala Ile Ser Lys Pro Glu Ala		
355	360	365
Glu Ile Glu Ser Ser Ser Glu Pro Glu Gly Ala His Ser Leu Trp Ile		
370	375	380
Ala Lys Asn Ala Gln Thr Thr Val Pro Met Val Asp Ile His Thr Ile		
385	390	395
Ser Val Asp Leu Ala Ser Phe Ser Ser Ser Gln Gln Glu Gly Thr Val		
405	410	415
Glu Ala Pro Gln Val Ile Val Pro Gly Gly Ser Tyr Val Arg Ser Gly		
420	425	430
Glu Leu Asn Leu Glu Leu Val Asn Thr Thr Gly Thr Gly Tyr Glu Asn		
435	440	445
His Ala Leu Leu Lys Asn Glu Ala Lys Val Pro Leu Met Ser Phe Val		
450	455	460
Ala Ser Ser Asp Glu Ala Ser Ala Glu Ile Ser Asn Leu Ser Val Ser		
465	470	475
Asp Leu Gln Ile His Val Ala Thr Pro Glu Ile Glu Glu Asp Thr Tyr		
485	490	495
Gly His Met Gly Asp Trp Ser Glu Ala Lys Ile Gln Asp Gly Thr Leu		
500	505	510
Val Ile Asn Trp Asn Pro Thr Gly Tyr Arg Leu Asp Pro Gln Lys Ala		
515	520	525

Gly Ala Leu Val Phe Asn Ala Leu Trp Glu Glu Gly Ala Val Leu Ser  
 530 535 540  
 Ala Leu Lys Asn Ala Arg Phe Ala His Asn Leu Thr Ala Gln Arg Met  
 545 550 555 560  
 Glu Phe Asp Tyr Ser Thr Asn Val Trp Gly Phe Ala Phe Gly Gly Phe  
 565 570 575  
 Arg Thr Leu Ser Ala Glu Asn Leu Val Ala Ile Asp Gly Tyr Lys Gly  
 580 585 590  
 Ala Tyr Gly Gly Ala Ser Ala Gly Val Asp Ile Gln Leu Met Glu Asp  
 595 600 605  
 Phe Val Leu Gly Val Ser Gly Ala Ala Phe Leu Gly Lys Met Asp Ser  
 610 615 620  
 Gln Lys Phe Asp Ala Glu Val Ser Arg Lys Gly Val Val Gly Ser Val  
 625 630 635 640  
 Tyr Thr Gly Phe Leu Ala Gly Ser Trp Phe Phe Lys Gly Gln Tyr Ser  
 645 650 655  
 Leu Gly Glu Thr Gln Asn Asp Met Lys Thr Arg Tyr Gly Val Leu Gly  
 660 665 670  
 Glu Ser Ser Ala Ser Trp Thr Ser Arg Gly Val Leu Ala Asp Ala Leu  
 675 680 685  
 Val Glu Tyr Arg Ser Leu Val Gly Pro Val Arg Pro Thr Phe Tyr Ala  
 690 695 700  
 Leu His Phe Asn Pro Tyr Val Glu Val Ser Tyr Ala Ser Met Lys Phe  
 705 710 715 720  
 Pro Gly Phe Thr Glu Gln Gly Arg Glu Ala Arg Ser Phe Glu Asp Ala  
 725 730 735  
 Ser Leu Thr Asn Ile Thr Ile Pro Leu Gly Met Lys Phe Glu Leu Ala  
 740 745 750  
 Phe Ile Lys Gly Gln Phe Ser Glu Val Asn Ser Leu Gly Ile Ser Tyr  
 755 760 765  
 Ala Trp Glu Ala Tyr Arg Lys Val Glu Gly Gly Ala Val Gln Leu Leu  
 770 775 780  
 Glu Ala Gly Phe Asp Trp Glu Gly Ala Pro Met Asp Leu Pro Arg Gln  
 785 790 795 800  
 Glu Leu Arg Val Ala Leu Glu Asn Asn Thr Glu Trp Ser Ser Tyr Phe  
 805 810 815  
 Ser Thr Val Leu Gly Leu Thr Ala Phe Cys Gly Gly Phe Thr Ser Thr  
 820 825 830  
 Asp Ser Lys Leu Gly Tyr Glu Ala Asn Thr Gly Leu Arg Leu Ile Phe  
 835 840 845

&lt;210&gt; 193

&lt;211&gt; 778

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

<400> 193  
 Met His His His His His Gly Leu Ala Ser Cys Val Asp Leu His  
 1 5 10 15  
 Ala Gly Gly Gln Ser Val Asn Glu Leu Val Tyr Val Gly Pro Gln Ala  
 20 25 30  
 Val Leu Leu Leu Asp Gln Ile Arg Asp Leu Phe Val Gly Ser Lys Asp  
 35 40 45  
 Ser Gln Ala Glu Gly Gln Tyr Arg Leu Ile Val Gly Asp Pro Ser Ser  
 50 55 60

Phe Gln Glu Lys Asp Ala Asp Thr Leu Pro Gly Lys Val Glu Gln Ser  
65 70 75 80  
Thr Leu Phe Ser Val Thr Asn Pro Val Val Phe Gln Gly Val Asp Gln  
85 90 95  
Gln Asp Gln Val Ser Ser Gln Gly Leu Ile Cys Ser Phe Thr Ser Ser  
100 105 110  
Asn Leu Asp Ser Pro Arg Asp Gly Glu Ser Phe Leu Gly Ile Ala Phe  
115 120 125  
Val Gly Asp Ser Ser Lys Ala Gly Ile Thr Leu Thr Asp Val Lys Ala  
130 135 140  
Ser Leu Ser Gly Ala Ala Leu Tyr Ser Thr Glu Asp Leu Ile Phe Glu  
145 150 155 160  
Lys Ile Lys Gly Gly Leu Glu Phe Ala Ser Cys Ser Ser Leu Glu Gln  
165 170 175  
Gly Gly Ala Cys Ala Ala Gln Ser Ile Leu Ile His Asp Cys Gln Gly  
180 185 190  
Leu Gln Val Lys His Cys Thr Thr Ala Val Asn Ala Glu Gly Ser Ser  
195 200 205  
Ala Asn Asp His Leu Gly Phe Gly Gly Ala Phe Phe Val Thr Gly  
210 215 220  
Ser Leu Ser Gly Glu Lys Ser Leu Tyr Met Pro Ala Gly Asp Met Val  
225 230 235 240  
Val Ala Asn Cys Asp Gly Ala Ile Ser Phe Glu Gly Asn Ser Ala Asn  
245 250 255  
Phe Ala Asn Gly Gly Ala Ile Ala Ala Ser Gly Lys Val Leu Phe Val  
260 265 270  
Ala Asn Asp Lys Lys Thr Ser Phe Ile Glu Asn Arg Ala Leu Ser Gly  
275 280 285  
Gly Ala Ile Ala Ala Ser Ser Asp Ile Ala Phe Gln Asn Cys Ala Glu  
290 295 300  
Leu Val Phe Lys Gly Asn Cys Ala Ile Gly Thr Glu Asp Lys Gly Ser  
305 310 315 320  
Leu Gly Gly Ala Ile Ser Ser Leu Gly Thr Val Leu Leu Gln Gly  
325 330 335  
Asn His Gly Ile Thr Cys Asp Lys Asn Glu Ser Ala Ser Gln Gly Gly  
340 345 350  
Ala Ile Phe Gly Lys Asn Cys Gln Ile Ser Asp Asn Glu Gly Pro Val  
355 360 365  
Val Phe Arg Asp Ser Thr Ala Cys Leu Gly Gly Ala Ile Ala Ala  
370 375 380  
Gln Glu Ile Val Ser Ile Gln Asn Asn Gln Ala Gly Ile Ser Phe Glu  
385 390 395 400  
Gly Gly Lys Ala Ser Phe Gly Gly Ile Ala Cys Gly Ser Phe Ser  
405 410 415  
Ser Ala Gly Gly Ala Ser Val Leu Gly Thr Ile Asp Ile Ser Lys Asn  
420 425 430  
Leu Gly Ala Ile Ser Phe Ser Arg Thr Leu Cys Thr Thr Ser Asp Leu  
435 440 445  
Gly Gln Met Glu Tyr Gln Gly Gly Ala Leu Phe Gly Glu Asn Ile  
450 455 460  
Ser Leu Ser Glu Asn Ala Gly Val Leu Thr Phe Lys Asp Asn Ile Val  
465 470 475 480  
Lys Thr Phe Ala Ser Asn Gly Lys Ile Leu Gly Gly Ala Ile Leu  
485 490 495  
Ala Thr Gly Lys Val Glu Ile Thr Asn Asn Ser Gly Gly Ile Ser Phe

500	505	510
Thr Gly Asn Ala Arg Ala Pro Gln Ala Leu Pro Thr Gln Glu Glu Phe		
	515	525
Pro Leu Phe Ser Lys Lys Glu Gly Arg Pro Leu Ser Ser Gly Tyr Ser	520	540
	530	535
Gly Gly Gly Ala Ile Leu Gly Arg Glu Val Ala Ile Leu His Asn Ala		555
	545	560
Ala Val Val Phe Glu Gln Asn Arg Leu Gln Cys Ser Glu Glu Ala	550	
	565	570
Thr Leu Leu Gly Cys Gly Gly Ala Val His Gly Met Asp Ser	580	590
	585	
Thr Ser Ile Val Gly Asn Ser Ser Val Arg Phe Gly Asn Asn Tyr Ala	595	605
	600	
Met Gly Gln Gly Val Ser Gly Gly Ala Leu Leu Ser Lys Thr Val Gln	610	620
	615	
Leu Ala Gly Asn Gly Ser Val Asp Phe Ser Arg Asn Ile Ala Ser Leu	625	640
	630	635
Gly Gly Gly Ala Leu Gln Ala Ser Glu Gly Asn Cys Glu Leu Val Asp	645	655
	650	
Asn Gly Tyr Val Leu Phe Arg Asp Asn Arg Gly Arg Val Tyr Gly Gly	660	670
	665	
Ala Ile Ser Cys Leu Arg Gly Asp Val Val Ile Ser Gly Asn Lys Gly	675	685
	680	
Arg Val Glu Phe Lys Asp Asn Ile Ala Thr Arg Leu Tyr Val Glu Glu	690	700
	695	
Thr Val Glu Lys Val Glu Glu Val Glu Pro Ala Pro Glu Gln Lys Asp	705	720
	710	715
Asn Asn Glu Leu Ser Phe Leu Gly Ser Val Glu Gln Ser Phe Ile Thr	725	735
	730	
Ala Ala Asn Gln Ala Leu Phe Ala Ser Glu Asp Gly Asp Leu Ser Pro	740	750
	745	
Glu Ser Ser Ile Ser Ser Glu Glu Leu Ala Lys Arg Arg Glu Cys Ala	755	765
	760	
Gly Gly Ala Asp Ser Ser Arg Ser Gly Cys	770	775

&lt;210&gt; 194

&lt;211&gt; 948

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;400&gt; 194

Met Ala Ser Met His His His His His His Val Lys Ile Glu Asn Phe	15
	1
	5
	10
Ser Gly Gln Gly Ile Phe Ser Gly Asn Lys Ala Ile Asp Asn Thr Thr	30
	20
	25
Glu Gly Ser Ser Ser Lys Ser Asn Val Leu Gly Gly Ala Val Tyr Ala	45
	35
	40
Lys Thr Leu Phe Asn Leu Asp Ser Gly Ser Ser Arg Arg Thr Val Thr	60
	50
	55
Phe Ser Gly Asn Thr Val Ser Ser Gln Ser Thr Thr Gly Gln Val Ala	80
	65
	70
	75
Gly Gly Ala Ile Tyr Ser Pro Thr Val Thr Ile Ala Thr Pro Val Val	95
	85
	90
Phe Ser Lys Asn Ser Ala Thr Asn Asn Ala Asn Asn Ala Thr Asp Thr	

100	105	110
Gln Arg Lys Asp Thr Phe Gly	Gly Ala Ile Gly Ala Thr Ser Ala Val	
115	120	125
Ser Leu Ser Gly Gly Ala His Phe Leu Glu Asn Val Ala Asp Leu Gly		
130	135	140
Ser Ala Ile Gly Leu Val Pro Asp Thr Gln Asn Thr Glu Thr Val Lys		
145	150	155
Leu Glu Ser Gly Ser Tyr Tyr Phe Glu Lys Asn Lys Ala Leu Lys Arg		
165	170	175
Ala Thr Ile Tyr Ala Pro Val Val Ser Ile Lys Ala Tyr Thr Ala Thr		
180	185	190
Phe Asn Gln Asn Arg Ser Leu Glu Glu Gly Ser Ala Ile Tyr Phe Thr		
195	200	205
Lys Glu Ala Ser Ile Glu Ser Leu Gly Ser Val Leu Phe Thr Gly Asn		
210	215	220
Leu Val Thr Pro Thr Leu Ser Thr Thr Thr Glu Gly Thr Pro Ala Thr		
225	230	235
Thr Ser Gly Asp Val Thr Lys Tyr Gly Ala Ala Ile Phe Gly Gln Ile		
245	250	255
Ala Ser Ser Asn Gly Ser Gln Thr Asp Asn Leu Pro Leu Lys Leu Ile		
260	265	270
Ala Ser Gly Gly Asn Ile Cys Phe Arg Asn Asn Glu Tyr Arg Pro Thr		
275	280	285
Ser Ser Asp Thr Gly Thr Ser Thr Phe Cys Ser Ile Ala Gly Asp Val		
290	295	300
Lys Leu Thr Met Gln Ala Ala Lys Gly Lys Thr Ile Ser Phe Phe Asp		
305	310	315
Ala Ile Arg Thr Ser Thr Lys Lys Thr Gly Thr Gln Ala Thr Ala Tyr		
325	330	335
Asp Thr Leu Asp Ile Asn Lys Ser Glu Asp Ser Glu Thr Val Asn Ser		
340	345	350
Ala Phe Thr Gly Thr Ile Leu Phe Ser Ser Glu Leu His Glu Asn Lys		
355	360	365
Ser Tyr Ile Pro Gln Asn Val Val Leu His Ser Gly Ser Leu Val Leu		
370	375	380
Lys Pro Asn Thr Glu Leu His Val Ile Ser Phe Glu Gln Lys Glu Gly		
385	390	395
Ser Ser Leu Val Met Thr Pro Gly Ser Val Leu Ser Asn Gln Thr Val		
405	410	415
Ala Asp Gly Ala Leu Val Ile Asn Asn Met Thr Ile Asp Leu Ser Ser		
420	425	430
Val Glu Lys Asn Gly Ile Ala Glu Gly Asn Ile Phe Thr Pro Pro Glu		
435	440	445
Leu Arg Ile Ile Asp Thr Thr Ser Gly Ser Gly Gly Thr Pro Ser		
450	455	460
Thr Asp Ser Glu Ser Asn Gln Asn Ser Asp Asp Thr Lys Glu Gln Asn		
465	470	475
Asn Asn Asp Ala Ser Asn Gln Gly Glu Ser Ala Asn Gly Ser Ser Ser		
485	490	495
Pro Ala Val Ala Ala Ala His Thr Ser Arg Thr Arg Asn Phe Ala Ala		
500	505	510
Ala Ala Thr Ala Thr Pro Thr Thr Pro Thr Ala Thr Thr Thr Thr		
515	520	525
Ser Asn Gln Val Ile Leu Gly Gly Glu Ile Lys Leu Ile Asp Pro Asn		
530	535	540

Gly Thr Phe Phe Gln Asn Pro Ala Leu Arg Ser Asp Gln Gln Ile Ser  
 545 550 555 560  
 Leu Leu Val Leu Pro Thr Asp Ser Ser Lys Met Gln Ala Gln Lys Ile  
 565 570 575  
 Val Leu Thr Gly Asp Ile Ala Pro Gln Lys Gly Tyr Thr Gly Thr Leu  
 580 585 590  
 Thr Leu Asp Pro Asp Gln Leu Gln Asn Gly Thr Ile Ser Ala Leu Trp  
 595 600 605  
 Lys Phe Asp Ser Tyr Arg Gln Trp Ala Tyr Val Pro Arg Asp Asn His  
 610 615 620  
 Phe Tyr Ala Asn Ser Ile Leu Gly Ser Gln Met Ser Met Val Thr Val  
 625 630 635 640  
 Lys Gln Gly Leu Leu Asn Asp Lys Met Asn Leu Ala Arg Phe Asp Glu  
 645 650 655  
 Val Ser Tyr Asn Asn Leu Trp Ile Ser Gly Leu Gly Thr Met Leu Ser  
 660 665 670  
 Gln Val Gly Thr Pro Thr Ser Glu Glu Phe Thr Tyr Tyr Ser Arg Gly  
 675 680 685  
 Ala Ser Val Ala Leu Asp Ala Lys Pro Ala His Asp Val Ile Val Gly  
 690 695 700  
 Ala Ala Phe Ser Lys Met Ile Gly Lys Thr Lys Ser Leu Lys Arg Glu  
 705 710 715 720  
 Asn Asn Tyr Thr His Lys Gly Ser Glu Tyr Ser Tyr Gln Ala Ser Val  
 725 730 735  
 Tyr Gly Gly Lys Pro Phe His Phe Val Ile Asn Lys Lys Thr Glu Lys  
 740 745 750  
 Ser Leu Pro Leu Leu Leu Gln Gly Val Ile Ser Tyr Gly Tyr Ile Lys  
 755 760 765  
 His Asp Thr Val Thr His Tyr Pro Thr Ile Arg Glu Arg Asn Gln Gly  
 770 775 780  
 Glu Trp Glu Asp Leu Gly Trp Leu Thr Ala Leu Arg Val Ser Ser Val  
 785 790 795 800  
 Leu Arg Thr Pro Ala Gln Gly Asp Thr Lys Arg Ile Thr Val Tyr Gly  
 805 810 815  
 Glu Leu Glu Tyr Ser Ser Ile Arg Gln Lys Gln Phe Thr Glu Thr Glu  
 820 825 830  
 Tyr Asp Pro Arg Tyr Phe Asp Asn Cys Thr Tyr Arg Asn Leu Ala Ile  
 835 840 845  
 Pro Met Gly Leu Ala Phe Glu Gly Glu Leu Ser Gly Asn Asp Ile Leu  
 850 855 860  
 Met Tyr Asn Arg Phe Ser Val Ala Tyr Met Pro Ser Ile Tyr Arg Asn  
 865 870 875 880  
 Ser Pro Thr Cys Lys Tyr Gln Val Leu Ser Ser Gly Glu Gly Glu  
 885 890 895  
 Ile Ile Cys Gly Val Pro Thr Arg Asn Ser Ala Arg Gly Glu Tyr Ser  
 900 905 910  
 Thr Gln Leu Tyr Pro Gly Pro Leu Trp Thr Leu Tyr Gly Ser Tyr Thr  
 915 920 925  
 Ile Glu Ala Asp Ala His Thr Leu Ala His Met Met Asn Cys Gly Ala  
 930 935 940  
 Arg Met Thr Phe  
 945

&lt;210&gt; 195

&lt;211&gt; 821

<212> PRT  
<213> Chlamydia

<400> 195  
Met His His His His His Glu Ala Ser Ser Ile Gln Asp Gln Ile  
1 5 10 15  
Lys Asn Thr Asp Cys Asn Val Ser Lys Val Gly Tyr Ser Thr Ser Gln  
20 25 30  
Ala Phe Thr Asp Met Met Leu Ala Asp Asn Thr Glu Tyr Arg Ala Ala  
35 40 45  
Asp Ser Val Ser Phe Tyr Asp Phe Ser Thr Ser Ser Gly Leu Pro Arg  
50 55 60  
Lys His Leu Ser Ser Ser Ser Glu Ala Ser Pro Thr Thr Glu Gly Val  
65 70 75 80  
Ser Ser Ser Ser Gly Glu Asn Thr Glu Asn Ser Gln Asp Ser Ala  
85 90 95  
Pro Ser Ser Gly Glu Thr Asp Lys Lys Thr Glu Glu Glu Leu Asp Asn  
100 105 110  
Gly Gly Ile Ile Tyr Ala Arg Glu Lys Leu Thr Ile Ser Glu Ser Gln  
115 120 125  
Asp Ser Leu Ser Asn Pro Ser Ile Glu Leu His Asp Asn Ser Phe Phe  
130 135 140  
Phe Gly Glu Gly Glu Val Ile Phe Asp His Arg Val Ala Leu Lys Asn  
145 150 155 160  
Gly Gly Ala Ile Tyr Gly Glu Lys Glu Val Val Phe Glu Asn Ile Lys  
165 170 175  
Ser Leu Leu Val Glu Val Asn Ile Ser Val Glu Lys Gly Gly Ser Val  
180 185 190  
Tyr Ala Lys Glu Arg Val Ser Leu Glu Asn Val Thr Glu Ala Thr Phe  
195 200 205  
Ser Ser Asn Gly Gly Glu Gln Gly Gly Gly Ile Tyr Ser Glu Gln  
210 215 220  
Asp Met Leu Ile Ser Asp Cys Asn Asn Val His Phe Gln Gly Asn Ala  
225 230 235 240  
Ala Gly Ala Thr Ala Val Lys Gln Cys Leu Asp Glu Glu Met Ile Val  
245 250 255  
Leu Leu Thr Glu Cys Val Asp Ser Leu Ser Glu Asp Thr Leu Asp Ser  
260 265 270  
Thr Pro Glu Thr Glu Gln Thr Lys Ser Asn Gly Asn Gln Asp Gly Ser  
275 280 285  
Ser Glu Thr Lys Asp Thr Gln Val Ser Glu Ser Pro Glu Ser Thr Pro  
290 295 300  
Ser Pro Asp Asp Val Leu Gly Lys Gly Gly Ile Tyr Thr Glu Lys  
305 310 315 320  
Ser Leu Thr Ile Thr Gly Ile Thr Gly Thr Ile Asp Phe Val Ser Asn  
325 330 335  
Ile Ala Thr Asp Ser Gly Ala Gly Val Phe Thr Lys Glu Asn Leu Ser  
340 345 350  
Cys Thr Asn Thr Asn Ser Leu Gln Phe Leu Lys Asn Ser Ala Gly Gln  
355 360 365  
His Gly Gly Gly Ala Tyr Val Thr Gln Thr Met Ser Val Thr Asn Thr  
370 375 380  
Thr Ser Glu Ser Ile Thr Thr Pro Pro Leu Val Gly Glu Val Ile Phe  
385 390 395 400  
Ser Glu Asn Thr Ala Lys Gly His Gly Gly Ile Cys Thr Asn Lys

405	410	415
Leu Ser Leu Ser Asn Leu Lys Thr Val Thr Leu Thr Lys Asn Ser Ala		
420	425	430
Lys Glu Ser Gly Gly Ala Ile Phe Thr Asp Leu Ala Ser Ile Pro Thr		
435	440	445
Thr Asp Thr Pro Glu Ser Ser Thr Pro Ser Ser Ser Pro Ala Ser		
450	455	460
Thr Pro Glu Val Val Ala Ser Ala Lys Ile Asn Arg Phe Phe Ala Ser		
465	470	475
Thr Ala Glu Pro Ala Ala Pro Ser Leu Thr Glu Ala Glu Ser Asp Gln		480
485	490	495
Thr Asp Gln Thr Glu Thr Ser Asp Thr Asn Ser Asp Ile Asp Val Ser		
500	505	510
Ile Glu Asn Ile Leu Asn Val Ala Ile Asn Gln Asn Thr Ser Ala Lys		
515	520	525
Lys Gly Gly Ala Ile Tyr Gly Lys Lys Ala Lys Leu Ser Arg Ile Asn		
530	535	540
Asn Leu Glu Leu Ser Gly Asn Ser Ser Gln Asp Val Gly Gly Leu		
545	550	555
Cys Leu Thr Glu Ser Val Glu Phe Asp Ala Ile Gly Ser Leu Leu Ser		560
565	570	575
His Tyr Asn Ser Ala Ala Lys Glu Gly Val Ile His Ser Lys Thr		
580	585	590
Val Thr Leu Ser Asn Leu Lys Ser Thr Phe Thr Phe Ala Asp Asn Thr		
595	600	605
Val Lys Ala Ile Val Glu Ser Thr Pro Glu Ala Pro Glu Glu Ile Pro		
610	615	620
Pro Val Glu Gly Glu Glu Ser Thr Ala Thr Glu Asn Pro Asn Ser Asn		
625	630	635
Thr Glu Gly Ser Ser Ala Asn Thr Asn Leu Glu Gly Ser Gln Gly Asp		640
645	650	655
Thr Ala Asp Thr Gly Thr Val Val Asn Asn Glu Ser Gln Asp Thr		
660	665	670
Ser Asp Thr Gly Asn Ala Glu Ser Gly Glu Gln Leu Gln Asp Ser Thr		
675	680	685
Gln Ser Asn Glu Glu Asn Thr Leu Pro Asn Ser Ser Ile Asp Gln Ser		
690	695	700
Asn Glu Asn Thr Asp Glu Ser Ser Asp Ser His Thr Glu Glu Ile Thr		
705	710	715
Asp Glu Ser Val Ser Ser Ser Lys Ser Gly Ser Ser Thr Pro Gln		720
725	730	735
Asp Gly Gly Ala Ala Ser Ser Gly Ala Pro Ser Gly Asp Gln Ser Ile		
740	745	750
Ser Ala Asn Ala Cys Leu Ala Lys Ser Tyr Ala Ala Ser Thr Asp Ser		
755	760	765
Ser Pro Val Ser Asn Ser Ser Gly Ser Asp Val Thr Ala Ser Ser Asp		
770	775	780
Asn Pro Asp Ser Ser Ser Ser Gly Asp Ser Ala Gly Asp Ser Glu Gly		
785	790	795
Pro Thr Glu Pro Glu Ala Gly Ser Thr Thr Glu Thr Pro Thr Leu Ile		800
805	810	815
Gly Gly Gly Ala Ile		
820		

<211> 525  
<212> PRT  
<213> Chlamydia

&lt;400&gt; 196

Met His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu  
1 5 10 15  
Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala  
20 25 30  
Ile Ala Gly Gln Ile Lys Leu Pro Thr Val His Ile Gly Pro Thr Ala  
35 40 45  
Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val  
50 55 60  
Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr  
65 70 75 80  
Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr  
85 90 95  
Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser  
100 105 110  
Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr  
115 120 125  
Leu Ala Glu Gly Pro Pro Ala Glu Phe Pro Leu Val Pro Arg Gly Ser  
130 135 140  
Pro Leu Pro Val Gly Asn Pro Ala Glu Pro Ser Leu Leu Ile Asp Gly  
145 150 155 160  
Thr Met Trp Glu Gly Ala Ser Gly Asp Pro Cys Asp Pro Cys Ala Thr  
165 170 175  
Trp Cys Asp Ala Ile Ser Ile Arg Ala Gly Tyr Tyr Gly Asp Tyr Val  
180 185 190  
Phe Asp Arg Val Leu Lys Val Asp Val Asn Lys Thr Phe Ser Gly Met  
195 200 205  
Ala Ala Thr Pro Thr Gln Ala Ile Gly Asn Ala Ser Asn Thr Asn Gln  
210 215 220  
Pro Glu Ala Asn Gly Arg Pro Asn Ile Ala Tyr Gly Arg His Met Gln  
225 230 235 240  
Asp Ala Glu Trp Phe Ser Asn Ala Ala Phe Leu Ala Leu Asn Ile Trp  
245 250 255  
Asp Arg Phe Asp Ile Phe Cys Thr Leu Gly Ala Ser Asn Gly Tyr Phe  
260 265 270  
Lys Ala Ser Ser Ala Ala Phe Asn Leu Val Gly Leu Ile Gly Phe Ser  
275 280 285  
Ala Ala Ser Ser Ile Ser Thr Asp Leu Pro Met Gln Leu Pro Asn Val  
290 295 300  
Gly Ile Thr Gln Gly Val Val Glu Phe Tyr Thr Asp Thr Ser Phe Ser  
305 310 315 320  
Trp Ser Val Gly Ala Arg Gly Ala Leu Trp Glu Cys Gly Cys Ala Thr  
325 330 335  
Leu Gly Ala Glu Phe Gln Tyr Ala Gln Ser Asn Pro Lys Ile Glu Met  
340 345 350  
Leu Asn Val Thr Ser Ser Pro Ala Gln Phe Val Ile His Lys Pro Arg  
355 360 365  
Gly Tyr Lys Gly Ala Ser Ser Asn Phe Pro Leu Pro Ile Thr Ala Gly  
370 375 380  
Thr Thr Glu Ala Thr Asp Thr Lys Ser Ala Thr Ile Lys Tyr His Glu  
385 390 395 400

<210> 197  
<211> 43  
<212> DNA  
<213> Chlamydia

<400> 197  
qataaggcgcg cccgcaatcat gaaattttatg tcagctactg ctg

43

<210> 198  
<211> 34  
<212> DNA  
<213> Chlamydia

<400> 198  
cagaacgcgt ttagaatgtc atacgagcac cgca

34

<210> 199  
<211> 6  
<212> DNA  
<213> Chlamydia

<400> 199  
gcaatc

<210> 200  
<211> 34  
<212> DNA  
<213> Chlamydia

<400> 200  
tgcaatcatg agttcgcaga aagatataaa aagc

34

<210> 201  
<211> 38  
<212> DNA  
<213> Chlamydia

<400> 201

cagagctagc taaaaagatc aatcgcaatc cagtattc 38  
<210> 202  
<211> 5  
<212> DNA  
<213> Chlamydia

<400> 202  
caatc 5  
  
<210> 203  
<211> 31  
<212> DNA  
<213> Chlamydia

<400> 203  
tgcaatcatg aaaaaagcgt ttttctttt c 31  
  
<210> 204  
<211> 31  
<212> DNA  
<213> Chlamydia

<400> 204  
cagaacgcgt ctagaatcgc agagcaattt c 31  
  
<210> 205  
<211> 30  
<212> DNA  
<213> Chlamydia

<400> 205  
gtgcaatcat gattcctcaa ggaatttacg 30  
  
<210> 206  
<211> 31  
<212> DNA  
<213> Chlamydia

<400> 206  
cagaacgcgt tttagaaccgg actttacttc c 31  
  
<210> 207  
<211> 50  
<212> DNA  
<213> Chlamydia

<400> 207  
cagacatatg catcaccatc accatcacga ggcgagctcg atccaagatc 50  
  
<210> 208  
<211> 40  
<212> DNA  
<213> Chlamydia

<400> 208  
cagaggtacc tcagatagca ctctctccta ttaaaggtagg 40

<210> 209  
<211> 55  
<212> DNA  
<213> Chlamydia

<400> 209  
cagagctagc atgcattacc atcaccatca cgtaaagatt gagaacttct ctggc 55

<210> 210  
<211> 35  
<212> DNA  
<213> Chlamydia

<400> 210  
cagaggtacc tttagaatgtc atacgagcac cgca 35

<210> 211  
<211> 36  
<212> DNA  
<213> Chlamydia

<400> 211  
cagacatatg catcaccatc accatcacgg gttac 36

<210> 212  
<211> 35  
<212> DNA  
<213> Chlamydia

<400> 212  
cagaggtacc tcagtcctc cagcacactc tcttc 35

<210> 213  
<211> 51  
<212> DNA  
<213> Chlamydia

<400> 213  
cagagctagc catcaccatc accatcacgg tgctatttct tgcttacgtg g 51

<210> 214  
<211> 38  
<212> DNA  
<213> Chlamydia

<400> 214  
cagaggtact taataagatca atcgaaatcc agtattcg 38

<210> 215  
<211> 48  
<212> DNA  
<213> Chlamydia

<400> 215  
cagaggatcc acatcacat caccatcacg gactagctag agaggttc 48

<210> 216  
<211> 31  
<212> DNA  
<213> Chlamydia

<400> 216  
cagagaattc ctagaatcgc agagcaattt c 31

<210> 217  
<211> 7  
<212> DNA  
<213> Chlamydia

<400> 217  
tgcaatc 7

<210> 218  
<211> 22  
<212> PRT  
<213> Chlamydia

<400> 218  
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Ser Ser Leu  
1 5 10 15  
Val Pro Ser Ser Asp Pro  
20

<210> 219  
<211> 51  
<212> DNA  
<213> Chlamydia

<400> 219  
cagaggtacc gcataccat caccatcaca tgattcctca aggaatttac g 51

<210> 220  
<211> 33  
<212> DNA  
<213> Chlamydia

<400> 220  
cagagcggcc gcttagaacc ggacttact tcc 33

<210> 221  
<211> 24  
<212> PRT  
<213> Chlamydia

<400> 221  
Met Ala Ser Met Thr Gly Gly Gln Gln Asn Gly Arg Asp Ser Ser Leu  
1 5 10 15

Val Pro His His His His His His  
20

<210> 222  
<211> 46  
<212> DNA  
<213> Chlamydia

<400> 222  
cagagcttagc catcaccatc accatcacct ctttggccag gatccc

46

<210> 223  
<211> 30  
<212> DNA  
<213> Chlamydia

<400> 223  
cagaactagt ctagaacctg taagtggtcc

30

<210> 224  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 224  
Met Ser Gln Lys Asn Lys Asn Ser Ala Phe Met His Pro Val Asn Ile  
1 5 10 15  
Ser Thr Asp Leu  
20

<210> 225  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 225  
Lys Asn Ser Ala Phe Met His Pro Val Asn Ile Ser Thr Asp Leu Ala  
1 5 10 15  
Val Ile Val Gly  
20

<210> 226  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 226  
His Pro Val Asn Ile Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly  
1 5 10 15  
Pro Met Pro Arg  
20

<210> 227  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 227  
Ser Thr Asp Leu Ala Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr  
1 5 10 15  
Glu Ile Val Lys  
20

<210> 228  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 228  
Val Ile Val Gly Lys Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys  
1 5 10 15  
Val Trp Glu Tyr  
20

<210> 229  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 229  
Gly Pro Met Pro Arg Thr Glu Ile Val Lys Lys Val Trp Glu Tyr Ile  
1 5 10 15  
Lys Lys His Asn  
20

<210> 230  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 230  
Ile Lys Lys His Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu  
1 5 10 15  
Pro Asp Ala Asn  
20

<210> 231  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 231  
Asn Cys Gln Asp Gln Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn  
1 5 10 15  
Leu Ala Lys Val  
20

<210> 232  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 232  
Lys Asn Lys Arg Asn Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe  
1 5 10 15  
Gly Ser Ser Asp  
20

<210> 233  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 233  
Ile Leu Pro Asp Ala Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro  
1 5 10 15  
Ile Asp Met Phe  
20

<210> 234  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 234

Asn Leu Ala Lys Val Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln  
1 5 10 15  
Met Thr Lys Ala  
20

<210> 235

<211> 22

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 235

Phe Gly Ser Ser Asp Pro Ile Asp Met Phe Gln Met Thr Lys Ala Leu  
1 5 10 15  
Ser Lys His Ile Val Lys  
20

<210> 236

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 236

Val Glu Ile Thr Gln Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro  
1 5 10 15  
Tyr Pro Val Glu  
20

<210> 237

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 237

Ala Val Pro Lys Tyr Ala Thr Val Gly Ser Pro Tyr Pro Val Glu Ile  
1 5 10 15  
Thr Ala Thr Gly  
20

<210> 238

<211> 20

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 238

Ala	Thr	Val	Gly	Ser	Pro	Tyr	Pro	Val	Glu	Ile	Thr	Ala	Thr	Gly	Lys
1															
														10	
															15

Arg	Asp	Cys	Val
		20	

&lt;210&gt; 239

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 239

Pro	Tyr	Pro	Val	Glu	Ile	Thr	Ala	Thr	Gly	Lys	Arg	Asp	Cys	Val	Asp
1															
														10	
															15

Val	Ile	Ile	Thr
		20	

&lt;210&gt; 240

&lt;211&gt; 21

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 240

Ile	Thr	Ala	Thr	Gly	Lys	Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln
1															
														10	
															15

Gln	Leu	Pro	Cys	Glu
		20		

&lt;210&gt; 241

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Made in a lab

&lt;400&gt; 241

Lys	Arg	Asp	Cys	Val	Asp	Val	Ile	Ile	Thr	Gln	Gln	Leu	Pro	Cys	Glu
1															
														10	
															15

Ala	Glu	Phe	Val
		20	

&lt;210&gt; 242

&lt;211&gt; 20

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

<220>  
<223> Made in a lab

<400> 242  
Asp Val Ile Ile Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg  
1 5 10 15  
Ser Asp Pro Ala  
20

<210> 243  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 243  
Thr Gln Gln Leu Pro Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala  
1 5 10 15  
Thr Thr Pro Thr  
20

<210> 244  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 244  
Cys Glu Ala Glu Phe Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala  
1 5 10 15  
Asp Gly Lys Leu  
20

<210> 245  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 245  
Val Arg Ser Asp Pro Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val  
1 5 10 15  
Trp Lys Ile Asp  
20

<210> 246  
<211> 20  
<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 246

Ala Thr Thr Pro Thr Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg  
1 5 10 15  
Leu Gly Gln Gly  
20

<210> 247

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 247

Ala Asp Gly Lys Leu Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu  
1 5 10 15  
Lys Ser Lys Ile  
20

<210> 248

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 248

Val Trp Lys Ile Asp Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr  
1 5 10 15  
Val Trp Val Lys  
20

<210> 249

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 249

Arg Leu Gly Gln Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro  
1 5 10 15  
Leu Lys Glu Gly  
20

<210> 250

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 250

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly  
1 5 10 15  
Cys Cys Phe Thr  
20

<210> 251

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 251

Gly Glu Lys Ser Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly  
1 5 10 15

<210> 252

<211> 12

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 252

Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly  
1 5 10

<210> 253

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 253

Gly Asp Lys Cys Lys Ile Thr Val Trp Val Lys Pro Leu Lys Glu Gly  
1 5 10 15

<210> 254

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 254  
Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala  
1 5 10 15  
Phe Gly Val Leu  
20

<210> 255  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 255  
Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn  
1 5 10 15  
Pro Glu Gly Ser  
20

<210> 256  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 256  
Phe Lys Ile Ser Glu Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu  
1 5 10 15  
Ala Leu Arg Ala  
20

<210> 257  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Made in a lab

<400> 257  
Ala Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr  
1 5 10 15  
Phe Leu Ile Asp  
20

<210> 258  
<211> 20  
<212> PRT  
<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 258

Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys  
1 5 10 15  
His Gly Val Ile  
20

<210> 259

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 259

Leu Ala Leu Arg Ala Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg  
1 5 10 15  
His Ala Val Ile  
20

<210> 260

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 260

Thr Phe Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn  
1 5 10 15  
Asp Leu Pro Leu  
20

<210> 261

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Made in a lab

<400> 261

Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly  
1 5 10 15  
Arg Ser Ile Asp  
20

<210> 262

<211> 20

<212> PRT

<213> Artificial Sequence

<220>  
 <223> Made in a lab

<400> 262  
 Arg His Ala Val Ile Asn Asp Leu Pro Leu Gly Arg Ser Ile Asp Glu  
 1 5 10 15  
 Glu Leu Arg Ile  
 20

&lt;210&gt; 263

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(897)

&lt;223&gt; n = A,T,C or G

<400> 263  
 atggcttcta tatgcggacg ttttaggtct ggtacaggga atgctctaaa agctttttt 60  
 acacagccca acaataaaaat ggcaagggtta gtaaataaga cgaaggagggt ggataagact 120  
 attaagggttg ccaagtctgc tgccgaaattg accgcaaata ttttggaaaca agctggaggc 180  
 gcgggctctt ccgcacacat tacagttcc caagtgtcca aaggattagg ggatgcgaga 240  
 actgttgtcg cttagggaa tgccttaac ggagcgttgc caggaacagt tcaaagtgcg 300  
 caaagcttct tctctcacat gaaagctgtc agtcayaaaa cgzaagaagg ggatgagggg 360  
 ctcacagcag atctttgtgt gtctcataag cgcagagcgg ctgcggctgt ctgtagcatc 420  
 atcggaggaa ttaccttaccc cgcgcacattc ggagctatcc gtccgattct gtttgtcaac 480  
 aaaatgctgg caaaaccgtt tctttttcc caaactaaag caaatatggg atcttctgtt 540  
 agctatatta tggcggttaa ccatgcagcg tctgtgggtgg gtgctgtact cgctatcagt 600  
 gcnnaaagag cagattgcg agcccgctgc gctcgatattt cgagagaaga gtgcgtactc 660  
 gaagtgcggg gagaggaaaaa tgcttgcgag aagaaagtcc ctggagagaa agccaagacg 720  
 ttacacgcga tcaagtatgc actcctact atgctcgaga agttttggg atgcgttgc 780  
 gacgtttca aatttgggtcc gctgcctatt acaatgggtt ttcgtgcgtat tggctgtct 840  
 ggatgtacgt tcacttctgc aattattggg ttgtgcactt tctgcgccag agcataa 897

&lt;210&gt; 264

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(298)

&lt;223&gt; Xaa = Any Amino Acid

<400> 264  
 Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu  
 1 5 10 15  
 Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn  
 20 25 30  
 Lys Thr Lys Gly Val Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala  
 35 40 45  
 Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser  
 50 55 60

Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg  
 65 70 75 80  
 Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr  
 85 90 95  
 Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln  
 100 105 110  
 Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser  
 115 120 125  
 His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile  
 130 135 140  
 Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn  
 145 150 155 160  
 Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met  
 165 170 175  
 Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val  
 180 185 190  
 Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala  
 195 200 205  
 Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly  
 210 215 220  
 Glu Glu Asn Ala Cys Glu Lys Val Ala Gly Glu Lys Ala Lys Thr  
 225 230 235 240  
 Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu  
 245 250 255  
 Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met  
 260 265 270  
 Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile  
 275 280 285  
 Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala  
 290 295

&lt;210&gt; 265

&lt;211&gt; 897

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(897)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 265

atggcttcta tatgcggacg tttagggtct ggtacaggga atgctctaaa agctttttt	60
acacagccca acaataaaaat ggcaagggtta gtaaataaga cgaaggaaat ggataagact	120
attaagggttgc caaagtctgc tgccgaattt accgcaaata ttttggaaaca agctggaggc	180
gcgggtctt ccgcacacat tacagttcc caagtgtcca aaggatttagg ggatgcgaga	240
actgttgtcg cttagggaa tgccttaac ggagcgttgc caggaacagt tcaaagtgcg	300
caaagttct tcttcacat gaaagctgct agtcagaaaaa cgcaagaagg ggatgagggg	360
ctcacagcag atctttgtgt gtctcataag cgccagagcgg ctgcggctgt ctgtacatc	420
atcgaggaa ttacctaccc cgccgacattc ggagctatcc gtccgattct gtttgtcaac	480
aaaatgtgg caaaaccgtt tctttttcc caaactaaag caaatatggg atcttctgtt	540
agctatatta tggcggtctaa ccatgcagcg tctgtgggg gtgctggact cgctatcagt	600
gcnnaagag cagattgcga agccccgtgc gctcgtattt cgagagaaga gtcgttactc	660
gaagtgcgg gagaggaaaa tgcttgcgag aagaaagtgc ctggagagaa agccaagacg	720
ttcacgcgca tcaagtatgc actcctcact atgctcgaga agtttttggg atgcgttgcc	780

gacgtttca aattggtgcc gctgcctatt acaaatggta ttctgtcgat tttggctgtc	840
ggatgtacgt tcacttctgc aattattgga ttgtgcactt tctgcgccag agcataa	897

&lt;210&gt; 266

&lt;211&gt; 298

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

&lt;220&gt;

&lt;221&gt; VARIANT

&lt;222&gt; (1)...(298)

&lt;223&gt; Xaa = Any Amino Acid

&lt;400&gt; 266

Met Ala Ser Ile Cys Gly Arg Leu Gly Ser Gly Thr Gly Asn Ala Leu			
1	5	10	15
Lys Ala Phe Phe Thr Gln Pro Asn Asn Lys Met Ala Arg Val Val Asn			
20	25	30	
Lys Thr Lys Gly Met Asp Lys Thr Ile Lys Val Ala Lys Ser Ala Ala			
35	40	45	
Glu Leu Thr Ala Asn Ile Leu Glu Gln Ala Gly Gly Ala Gly Ser Ser			
50	55	60	
Ala His Ile Thr Ala Ser Gln Val Ser Lys Gly Leu Gly Asp Ala Arg			
65	70	75	80
Thr Val Val Ala Leu Gly Asn Ala Phe Asn Gly Ala Leu Pro Gly Thr			
85	90	95	
Val Gln Ser Ala Gln Ser Phe Phe Ser His Met Lys Ala Ala Ser Gln			
100	105	110	
Lys Thr Gln Glu Gly Asp Glu Gly Leu Thr Ala Asp Leu Cys Val Ser			
115	120	125	
His Lys Arg Arg Ala Ala Ala Val Cys Ser Ile Ile Gly Gly Ile			
130	135	140	
Thr Tyr Leu Ala Thr Phe Gly Ala Ile Arg Pro Ile Leu Phe Val Asn			
145	150	155	160
Lys Met Leu Ala Lys Pro Phe Leu Ser Ser Gln Thr Lys Ala Asn Met			
165	170	175	
Gly Ser Ser Val Ser Tyr Ile Met Ala Ala Asn His Ala Ala Ser Val			
180	185	190	
Val Gly Ala Gly Leu Ala Ile Ser Ala Xaa Arg Ala Asp Cys Glu Ala			
195	200	205	
Arg Cys Ala Arg Ile Ala Arg Glu Glu Ser Leu Leu Glu Val Pro Gly			
210	215	220	
Glu Glu Asn Ala Cys Glu Lys Lys Val Ala Gly Glu Lys Ala Lys Thr			
225	230	235	240
Phe Thr Arg Ile Lys Tyr Ala Leu Leu Thr Met Leu Glu Lys Phe Leu			
245	250	255	
Glu Cys Val Ala Asp Val Phe Lys Leu Val Pro Leu Pro Ile Thr Met			
260	265	270	
Gly Ile Arg Ala Ile Val Ala Ala Gly Cys Thr Phe Thr Ser Ala Ile			
275	280	285	
Ile Gly Leu Cys Thr Phe Cys Ala Arg Ala			
290	295		

&lt;210&gt; 267

&lt;211&gt; 680

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 267

tctatatacca tattgatagg	aaaaaaacgtc	gcagaaaagat	tttagctatg	acgtttatcc	60
gagctttagg	atattcaaca	gatgcagata	ttattgaaga	gttctttct	120
gttccttacg	ttcagagaag	gattttgctg	cgttagttgg	taaagttaa	180
tagttgatgc	ggattcttca	ttagttacg	ggaaagctgg	agagaagcta	240
tgctaaaacg	catcttagat	acgggagtc	aatcttgaa	gattgctgtt	300
aaaatcaccc	aattattaag	atgctcgcaa	aagatcctac	ggattcttac	360
ttaaagattt	ttatcgaga	ttacgaccag	gagagcctgc	aactttagct	420
ccacaattat	gcgttatttc	ttcgatgcta	aacgttataa	tttaggccgc	480
ataaattaaa	taaaaaattt	ggcttcccat	tagacgacga	aacattatct	540
tgagaaaaya	agatgttattc	ggcgegttga	aatatttgat	tcgtttgcga	600
agaagacatc	tatcgatgat	attgaccatt	tggcaaaccg	acgagttcgc	660
aactaattca	gaatcactgt				680

&lt;210&gt; 268

&lt;211&gt; 359

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 268

cttatgttct	ggagaatgtt	gcaacaacat	attaatcgaa	ccagctccctc	60
agaaacccaag	ccctttttag	aaaaaacctg	tacttcgcac	ccttttagcca	120
agctcctaac	aaagagctaa	tttttcctc	ttccttggtt	ttctgaggcg	180
taaatatagc	aagtgcctt	gyaacaccc	atcaacaatc	gttgtccta	240
agagactgtc	tctccatcaa	ttaaatggag	tttcaaagta	atatccccctt	300
atcacaagac	tctatgaaag	ctatctgatt	ccatcgagca	ggatgtatg	359

&lt;210&gt; 269

&lt;211&gt; 124

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 269

gatcaaatca	attgagggag	ctcattaaca	agaatagctg	cagtttttttgcgttcttct	60
ggaataacaa	gaaataggtt	atcggtacca	ttgatagaac	gaacacgaca	120
ggtt					124

&lt;210&gt; 270

&lt;211&gt; 219

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 270

gatccgttg	ggcctagtaa	taatacgttg	gatttccat	aactcacttg	60
ataagagcac	ggatacgtt	atagtgtt	tagacggcaa	ccgaaatcgt	120
cgctttgtc	caatgacata	agagtcgatg	tggcgtttg	tttctttagg	180
ctcagacttg	ttggagagct	tgtggaagat	gttgcgatc	gtttaacact	219

&lt;210&gt; 271

&lt;211&gt; 511

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

<220>

<221> misc\_feature

<222> (1) ... (511)

<223> n = A,T,C or G

<400> 271  
 ggatccaat tcggcacgag gagaaaatat aggaggttcc akcatcgaa gatctaata 60  
 acaaagaggt tttgcataat atggctccctt cttgtacgtt caacgatgtat tggaggat 120  
 tgtagatcgat agcttggttc ccagagaact gacaagtccc gctacattga gagaatgtaa 180  
 cctgttctcc atagatagct cctcctacta cacctgaata agttgggtt gctggagatg 240  
 atggtgccgc tgctgcggct gctttaggg aagcagcgc tgcagcaggt gctgaagctg 300  
 ttgtgcgac tcctgtggat gaggagttt cttgttggat cgagaaagag aagctgatt 360  
 tcagattaga atatattaca gtttttagcat gtaagcctcc accttccttc ccaacaagg 420  
 tctctgttac agataaggag actagangca tctagttttt aagattttt acagcagata 480  
 cctccaccta tctctgttagc ggagttctca g 511

<210> 272  
<211> 598  
<212> DNA  
<213> Chlamydia

<400> 272  
 ctcttcctct cctcaatcta gttctggagc aactacagtc tccgactcag gagactctag 60  
 ctctggctca aactcgata cctaaaaac agttccagtc acagctaaag gcgggtggct 120  
 ttatactgtat aagaatcttt cgattactaa catcacagga attatcgaaa ttgcaaaataa 180  
 caaagcgaca gatgttggag gtgggtctta cgtaaaagga acccttactt gtaaaaaactc 240  
 tcaccgtcta caatttttga aaaactcttc cgataaaacaa ggtggaggaa tctacggaga 300  
 agacaacatc accctatcta atttgacagg gaagactcta ttccaagaga atactgccaa 360  
 aaaagagggc ggtggactct tcataaaagg tacagataaa gctttacaa tgacaggact 420  
 ggatagtttc tggttaatta ataacacatc agaaaaacat ggtggggaa gcctttgtta 480  
 ccaaagaaat ctctcagact tacacctttt gatgtggaaa caattccagg aatcacgcct 540  
 gtacatggtg aaacagtcat tactggcaat aaatctacag gagtaatgg tggaggc 598

<210> 273  
<211> 126  
<212> DNA  
<213> Chlamydia

<400> 273  
 ggtatccaat tcggcacgag atgaggctta tagtttaca aaagcttctc acatttccttc 60  
 gatagctttt tattagccgt ttttagcatc ctaatgagat ctccctcggtt gtaacaata 120  
 cgagag 126

<210> 274  
<211> 264  
<212> DNA  
<213> Chlamydia

<400> 274  
 ggatccaat tcggcacgag ctctttaaa tcttaattac aaaaagacaa attaattcaa 60  
 tttttcaaaa aagaattaa acattaatttgg ttgtaaaaaaaaa acaatattta ttctaaaata 120  
 ataaccatag ttacggggaa atctttca tggtttattt tagagctcat caaccttaggc 180  
 atacgcctaa aacatttcct ttgaaagttc accattcggtt ctccgataag catcctcaaa 240  
 ttgctaaagc tatgtggatt acgg 264

<210> 275  
<211> 359  
<212> DNA  
<213> Chlamydia

<400> 275  
ggatccgaat tcggcacgag ataaaacctg aaccacaaca aagatctaaa acttcttgat 60  
tttcagctgc aaattcttt agataaatat caaccatttc ttcaagttca tatcttgaa 120  
ttaaaacttg ttctcttaaa ttaattcttag tatttaagtta ttcaacatag cccattatta 180  
attgaattgg ataattttgc cttataattt cacattctt ttcaagttcaatt tttaggttcta 240  
aacgtaccg cttttttctt aaaattaatg ttcttcattt attcatat taagccactt 300  
tccttattt tttgattttg ttctctgtt agtaatgctt caataatagt taataat 359

<210> 276  
<211> 357  
<212> DNA  
<213> Chlamydia

<400> 276  
aaaacaattg atataatttt tttttcata acttccagac tcctttctag aaaagtcttt 60  
atgggttagta gtgactctaa cgaaaaatc tttcgccaga aacttttagca ctattaaaga atcgttacgg 120  
ttagataag ctttattca cccagtatct tatctatttg aaatgtctgc taacactaga 180  
tttcgggaa tctttatct acaaagatcg aatctcago attattgtctg ccgtcttcc 240  
atcttccgtt attcttggac ttgaaagctt gtgtttactc gtgccgaatt cgatcc 300  
357

<210> 277  
<211> 505  
<212> DNA  
<213> Chlamydia

<400> 277  
ggatccgaat tcggcacgag ctcgtccccga ttgcttgctt cagtcacccc atcggtata 60  
agcactaaaa gagactccctt ttcaagaacg agagtgtaa cagggtgagg aggaacttca 120  
ggtaaaaaatc ctaaggccat accaggatgc gacaggaaag agatatctcc attaggagct 180  
cgagacacg ctgggttgc gcccacaagaa tagtattcta gttctcggt tgctaatga 240  
taacaataaa tgcatagtgt tacaaacatc ccagattcag ctgtctgtg atagaagaga 300  
gcagctgtt gttgaacggc ttcttgcata gaggagagct cactaaaaaa ggtatgtaac 360  
atgttttca ggaataagga gttaggcgcac gcattgactc cttccggaa agcatcagca 420  
acgattagaa agagtttgc ttggggacct tcgcctataa caaagatatc aaagaaatct 480  
cctccctaccg taactgcagg aatat 505

<210> 278  
<211> 407  
<212> DNA  
<213> Chlamydia

<400> 278  
ggatccgaat tcggcacgag aactactgag caaattgggt atccaacttc ctctttacga 60  
aagaaaaaca gaaggcattc tccataccaa gatttggc atcgacaata aaactccaaat 120  
ctttggctct gctaaactggc gcggtgctgg tatgattaaa aactttgaag acctattcat 180  
ccttcggccca attacagaga cacagttca ggccctttag gacgtctggc ctcttctaga 240  
aacaatagc tcctatctgt ccccagagag cgtgcttacg gcccctactc cttcaagtag 300  
acctactcaa caagatacag attctgtatga cgaacaaccg agtaccagcc agcaagctat 360

ccgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca	407
<210> 279	
<211> 351	
<212> DNA	
<213> Chlamydia	
<400> 279	
ctcgtgccgc ttacaggagg cttgtatcct taaaataga gttttctta tgaccccatg	60
tggcgatagg ccgggtctag cgccgatagt agaaatatcg gttgggtttt gtccttgagg	120
ggatcgata cttttcaaa gtatggccc cgatcgatt atctggagc tcttatgtct	180
tttttccata cttagaaaata taagttatc ctcagaggac tcttgtt agcaggctgt	240
ttcttaatga acagctgttc ctctagtcga gggaaatcaac ccgctgatga gagcatctat	300
gtcttgtcta tgaatcgat gatttgtat tctcgtgccg aattcgatc	351
<210> 280	
<211> 522	
<212> DNA	
<213> Chlamydia	
<400> 280	
ggatccgaat tcggcacgag cagaggaaaa aggcyatact cctcttgaag atcgtttac	60
agaagatctt tccgaagtct ctggagaaga ttttcgagga ttgaaaaatt cgttcgatga	120
tgattttct tctgacgaaa ttctcgatgc gtcacaagt aaattttctg atcccacaat	180
aaagatcta gctttgatt atctaattca aatagctccc tctgatggaa aacttaagtc	240
cgtctcatt caggcaaaagc atcaactgat gageragaat cctcaggcga ttgttggagg	300
acgcaatgtt ctgttagctt cagaaacctt tgcgtccaga gcaaatacat ctccctcatc	360
gcttcgtcc ttatatttcc aagtaacctc atccccctt aattgcgcta atttacatca	420
aatgccttgc tcttactcgc catcagagaa aaccgtgtt atggagttt tagtgaatgg	480
catggtagca gatttaaat cggaggccc ttccatctt cc	522
<210> 281	
<211> 577	
<212> DNA	
<213> Chlamydia	
<400> 281	
ggatccgaat tcggcacgag atgcttctat tacaattggg ttggatgcgg aaaaagctta	60
ccagcttatt cttagaaaagt tgggagatca aattcttggg ggaatttgcgt atactattgt	120
tgatagtaca gtccaagata ttttagacaa aatcacaaca gacccttctc taggtttgtt	180
gaaagctttt aacaacttcc caatcaactaa taaaattcaa tgcaacgggt tattcactcc	240
caggaacatt gaaactttat taggaggaac tgaatagga aaattcacag tcacacccaa	300
aagctctggg agcatgttct tagtctcagc agatattatt gcatcaagaa tggaaaggcgg	360
cgttggctca gctttggatc gagaaggtga ttctaaagccc tacgcgatta gttatggata	420
ctcatcaggc gttcctaatt tatgtatgtt aagaaccaga attattaata caggattgac	480
tccgacaacg tattcattac gtgttaggcgg ttttagaaacg ggtgtgttat gggtaatgc	540
ccttctaat ggcaatgata ttttaggaat aacaaat	577
<210> 282	
<211> 607	
<212> DNA	
<213> Chlamydia	
<400> 282	
actmatcttc cccgggctcg agtgcggccg caagcttgc gacggagctc gataaaaaaa	60

tgtgtgcgtg tgaaccgctt cttcaaaagc ttgtcttaaa agatattgtc tcgcttcgg	120
attagttaca tgaaaaaaa ttgctagaac aatattattc ccaaccaagc tctctgcgg	180
gctaaaaaaa cctaaattca aaagaatgac tcgcccgtca tcttcagaaa gacgatccga	240
cttccataat tcgatgtctt tccccatggg gatctctgtc gggagccagt tatttgcga	300
gccatcaaa taatgttccc aagcccattt gtacttaata ggaacaagtt ggttgacatc	360
gacctggttg cagttacta gacgctgtc atttagatta acgcgttct gtttccatc	420
taaaatatct gcttgataa gaaccgttaa ttttattgtt aatttatatg attaattact	480
gacatgttc acacccttct tccaaagaac agacagggtc tttctcgct cttaaccaa	540
taattctgc cgaaggcagac ttattttca tccaaacgagg ctgaattctt cttttattaa	600
tatctac	607

&lt;210&gt; 283

&lt;211&gt; 1077

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 283

ggatccgaat tcggcacgag aagttaacga tgacgatttg ttcccttggg agagaaggag	60
caatcgaaac taaaatgtcg agagcatgtg aagactccaa tgcaggaata atcccctcat	120
ttcttagtaag caggaaaaaa gctcgtaacg cctcttcattc ggtggctaat gtataaaagg	180
ctcgctctga ctcatgcatt tcggcatgtat ctggcccaac tgaaggataa tctaattccag	240
cggaaatggaa gtgagtttgt aataactgtc catcgatcattc ttcgaagaaga tacgaataaa	300
atccgtggaa tactccaggt cgccctgttgc caaaacgtgc tgcattttt cctgaagaaa	360
tgcccagtcc tcccccttcc actccaattt attggacttt tggattcggg ataaaaatgat	420
ggaaaaatcc aatacggttgc gagccacccctc cgtatcatgc aatcagaata tcaggatctc	480
ttccctgcAAC tgcattggatt tgctttca cttcagcgct tataacagac tggaaaaatcc	540
gaacgatatac gggataaggtaa agggccatcc taagcaatag tgagtaaatg	600
agtgtgttgt tgcccaatct tgtagagctt gattaactgc atctttgagt ccacaagatc	660
cttttggtaac agaaacgact tcagcaccta aaaagcgcat ttctctaca tttggttct	720
gtcqgtccac atctttgtc cccatgtata ctacacatac taatccataga taagcacacg	780
ctgttgcgt tgctactcga tggtgtcccg cacctgttgc agctacaaca cgtgtttcc	840
caagatattt agcaagcaaa cactgaccaa gacgttattt cagttatgt gctccgtat	900
gaaaaagatc ttgcgttta agaaatactc tagggccatc aatagctcg acaaaaattct	960
taacttcagt cagaggagt tgctccccg catagttttt caaaaatacaa totagttcag	1020
ataaaaaact ttgctgagtt ttgagaatct cccattccgc ttttagattc tgtatag	1077

&lt;210&gt; 284

&lt;211&gt; 407

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

&lt;400&gt; 284

ggatccgaat tcggcacgag aactactgag caaattgggt atccaacttc ctcttacga	60
aagaaaaaca gaaggcattc tccatccaa gatttggc atcgacaata aaactccaaat	120
ctttggctct gctaactggc gcgggtgtgg tatgattaaa aactttgaag acctattcat	180
ccttcggccaa attacagaga cacagctca ggcctttatg gacgtctgg ctcttctaga	240
aacaataggcc tcctatctgt cccccagagag cgtgtttacg gcccctactc cttcaagtag	300
acctactcaa caagatacag attctgtatgc cgaacaaccg agtaccagcc agcaagctat	360
ccgtatgaga aaataggatt agggaaacaa aacgacagca aaccaca	407

&lt;210&gt; 285

&lt;211&gt; 802

&lt;212&gt; DNA

&lt;213&gt; Chlamydia

<400> 285  
 ggtatccaat tcggcacgag ttagcttaat gtcttgcgtca tctctaccta catttgcagc 60  
 taattctaca ggcacaattt gaatcgtaa ttacgtcg tgcctagaag agtctgtct 120  
 tggaaaaaaa gaatctgctg aattcgaaaa gatggaaaaac caattctctt acagcatggg 180  
 gaagatggag gaagaactgt ctctatcta ttccaagctc caagacgacg attacatgga 240  
 aggcttatcc gagaccgca gtcggaaatt aagaaaaaaa ttcaagatc tatctgcaga 300  
 atacaacaca gctcaaggcc agtattacca aatattaaac caaagtaatc tcaagcgcat 360  
 gcaaaagatt atggaagaag tgaaaaaagc ttctgaaact gtgcgtattc aagaaggctt 420  
 gtcagtccctt cttacgaaat atattgtctt atctatcgat agttcggcag ataaaaccga 480  
 tgctgttatt aaagttcttg atgattctt tcaaaataat taacatgcga agctagccga 540  
 ggagtgccgt atgtctcaat ccacttattc tcttgaacaa ttagctgatt tttgaaagt 600  
 cgagttcaa gaaaaatggag ctactttct ttccggagtt gaagagatcg aggaagcaa 660  
 aacggcacac atcacattct tagataatga aaaatatgct aaacattaa aatcatcgga 720  
 agctggcgct atcatcatat ctgcacaca gttcaaaaaa tatcgagact tgaataaaaa 780  
 ctttcttatac acttctgagt ct 802

<210> 286  
<211> 588  
<212> DNA  
<213> Chlamydia

<400> 286  
 ggtatccaat tcggcacgag gcaatattta ctcccaacat tacggttcca aataagcgat 60  
 aaggcttctt aataaggaag ttaatgttaag aggtttttt attgctttt gtaaggtgt 120  
 attgcaaccg cacgcgtt aatgatacgc aagccatttc catcatyggaa sagaaccctt 180  
 ggacaaaaat acaaaggagg ttcaacttta accagaaaaa gggagayttt gttccatgg 240  
 gttttccctt tatacaccctt ttccacacaa ttaggagccg cgtctgtat tggaaataca 300  
 aattgtcccc aagcgaattt tggctctgtt tcagggttt ctccataattt ttcgtcagc 360  
 catccgccta tggtaacgca attagctgtt gtaggaagat caactccaaa caggtcatag 420  
 aaatcagaaa gctcatatgtt gcctgcagca ataacaacat tcttgcgtga gtgagcgaat 480  
 tggtaatca atccttctat agacccatat tcatcaatga taatctcg 540  
 tggtaatca atccttctat agacccatat tcatcaatga taatctcg 588

<210> 287  
<211> 489  
<212> DNA  
<213> Chlamydia

<220>  
<221> misc\_feature  
<222> (1)...(489)  
<223> n = A,T,C or G

<400> 287  
 agtgcctatt gtttgcagg ctttgcgtga tgatagcgat accgtacgtg agattgtgt 60  
 acaagtagct gttatgtatg gttctagttt cttactgcgc gcccgtggcg atttagcgaa 120  
 aaatgattct tctattcaag tacgcacac tgcattatcgat gtcgcagccg tggatggat 180  
 acaagatctt gtgcctcatt tacgagttt agtccaaaat acacaattag atgaaacgga 240  
 aagaagagaa gcttggagat ctttatgtt tcttactcgg cctcatagtg gtgtattaac 300  
 tggcatagat caagctttaa tgacctgtga gatgtttaaag gaatatcctg aaaagtgtac 360  
 ggaagaacag attcgtacat tattggctgc agatcatcca gaagtgcagg tagtacttt 420  
 acagatcatt ctgagaggag gtagagtatt ccggcatct tctataatgg aatcggttct 480  
 cgtgccnt 489

<210> 288

<211> 191  
<212> DNA  
<213> Chlamydia

<400> 288  
ggatccgaat tcaggaatatg ctgtgggtt atcaataaaa agggtttgc catttttaa 60  
gacgactttg tagataaacgc taggagctgt agcaataata tcgagatcaa attctctaga 120  
gattctctca aagatgattt ctaagtgcag cagtcctaaa aatccacagc ggaacccaaa 180  
tccgagagag t 191

<210> 289  
<211> 515  
<212> DNA  
<213> Chlamydia

<400> 289  
ggatccgaat tcggcacgag gagcgcacgtg aaatagtgga atcttcccgt attcttatta 60  
cttctgcgtt gccttacgca aatggtcctt tgcattttgg acatattacc ggtgcttattt 120  
tgcctgcaga tgggttatgcg cggtttcaga gactacaagg caaagaggtt ttgtatattt 180  
gtgggtctga tgaatacggg atcgcaatta cccttaatgc agagttggca ggcatggggt 240  
atcaagaata tgcgcacatg tatcataaaggc ttcataaaga taccttcaag aaattgggaa 300  
tttctgtaga tttcttttcc agaactacgaa acgcttatca tcctgttattt gtgcagattt 360  
tctatcgaaa cttgcaggaa cgcggactgg tagagaatca ggtgaccgaa cagctgttattt 420  
ctgaggaaga agggaaagttt ttagcggacc gttatgtt tott aggtacttgtt cccaaatgtt 480  
ggtttgcgtt agctcgagggaa gatgagtgcc agcag 515

<210> 290  
<211> 522  
<212> DNA  
<213> Chlamydia

<400> 290  
ggatccgaat tcggcacgag ggaggaatgg aaggggccctc cgattktama tctgcttacca 60  
tgccattcac tagaaactcc ataacagcgg ttttctctga tggcgagtaa gaagcaagca 120  
tttgcgtt aatcgccaa ttagggggg atgagggttac ttggaaatat aaggagcggaa 180  
gcgtgttgcg aggatgttattt gctctggaa caaagggttcc tgaagctaac agaacattgc 240  
gtcctccaac aatcgccctga ggattctggc tcatcgttgc atgcatttgc tgaatggag 300  
cgacttaag tttccatca gagggagcta ttgaatttag ataatcaaga gctagatcc 360  
ttattgtggg atcagaaaaat ttacttgcgaa ggcgcatttgc aatttcgtca gaagaagaat 420  
catcatcgaa cgaatttttc aatcctcgaa aatcttctcc agagacttgc gaaagatctt 480  
ctgtgaaacg atcttcaaga ggagtatcgc cttttccyc tg 522

<210> 291  
<211> 1002  
<212> DNA  
<213> Chlamydia

<400> 291  
atggcgacta acgcaatttgc atcggcagga agtgcagcaaa gtaagatgt gctgccagtt 60  
gccaagaac cagcggctgt cagctccctt gctcagaaag ggattttattt tattcaacaa 120  
ttttttacaa accctggaa taagtttagca aagttttagt gggcaacaaa aagtttagat 180  
aaatgcctta agctaagtaa ggcggtttgc gactgtgtcg taggatcgtt ggaagaggcg 240  
ggatgcacag gggacgcattt gacccctcgcc agaaaacgccc agggatgtt aaaaacaact 300  
cgagaagtttgc ttgccttagc taatgtgtc aatggagctg ttccatctat cgttaactcg 360  
actcagaggtt gttaccaata cacacgtcaaa gccttcgagt taggaagcaaa gacaaaagaa 420

agaaaaaacgc	ctggggagta	tagtaaaatg	ctattaactc	gaggtgatta	cctattggca	480
gcttcaggg	aagcttgtac	ggcagtcggt	gcaacgactt	actcagcgac	attcggtgtt	540
ttacgtccgt	taatgttaat	caataaaactc	acagcaaaac	cattcttaga	caaagcgact	600
gtaggcaatt	ttggcacggc	tgttgctgga	attatgacca	ttaatcatat	ggcaggagtt	660
gctggtgctg	ttggcggaaat	cgcattagaa	caaaagctgt	tcaaacgtgc	gaaggaatcc	720
ctatacaatg	agagatgtgc	cttagaaaac	caacaatctc	agttgagtgg	ggacgtgatt	780
ctaagcgcgg	aaagggcatt	acgtaaaagaa	cacgttgcta	ctctaaaaag	aatgtttta	840
actcttcttgc	aaaaagctt	agagttgta	gtggatggag	tcaaactcat	tccttaccg	900
attacagtgg	cttgctccgc	tgcaatttct	ggagccttga	cggcagcatc	cgcaggaatt	960
ggcttatata	gcatatggca	gaaaacaag	tctggcaaat	aa		1002

&lt;210&gt; 292

&lt;211&gt; 333

&lt;212&gt; PRT

&lt;213&gt; Chlamydia

<400> 292						
Met Ala Thr Asn Ala Ile Arg Ser Ala Gly Ser Ala Ala Ser Lys Met						
1	5	10	15			
Leu Leu Pro Val Ala Lys Glu Pro Ala Ala Val Ser Ser Phe Ala Gln						
20	25	30				
Lys Gly Ile Tyr Cys Ile Gln Gln Phe Phe Thr Asn Pro Gly Asn Lys						
35	40	45				
Leu Ala Lys Phe Val Gly Ala Thr Lys Ser Leu Asp Lys Cys Phe Lys						
50	55	60				
Leu Ser Lys Ala Val Ser Asp Cys Val Val Gly Ser Leu Glu Glu Ala						
65	70	75	80			
Gly Cys Thr Gly Asp Ala Leu Thr Ser Ala Arg Asn Ala Gln Gly Met						
85	90	95				
Leu Lys Thr Thr Arg Glu Val Val Ala Leu Ala Asn Val Leu Asn Gly						
100	105	110				
Ala Val Pro Ser Ile Val Asn Ser Thr Gln Arg Cys Tyr Gln Tyr Thr						
115	120	125				
Arg Gln Ala Phe Glu Leu Gly Ser Lys Thr Lys Glu Arg Lys Thr Pro						
130	135	140				
Gly Glu Tyr Ser Lys Met Leu Leu Thr Arg Gly Asp Tyr Leu Leu Ala						
145	150	155	160			
Ala Ser Arg Glu Ala Cys Thr Ala Val Gly Ala Thr Thr Tyr Ser Ala						
165	170	175				
Thr Phe Gly Val Leu Arg Pro Leu Met Leu Ile Asn Lys Leu Thr Ala						
180	185	190				
Lys Pro Phe Leu Asp Lys Ala Thr Val Gly Asn Phe Gly Thr Ala Val						
195	200	205				
Ala Gly Ile Met Thr Ile Asn His Met Ala Gly Val Ala Gly Ala Val						
210	215	220				
Gly Gly Ile Ala Leu Glu Gln Lys Leu Phe Lys Arg Ala Lys Glu Ser						
225	230	235	240			
Leu Tyr Asn Glu Arg Cys Ala Leu Glu Asn Gln Gln Ser Gln Leu Ser						
245	250	255				
Gly Asp Val Ile Leu Ser Ala Glu Arg Ala Leu Arg Lys Glu His Val						
260	265	270				
Ala Thr Leu Lys Arg Asn Val Leu Thr Leu Leu Glu Lys Ala Leu Glu						
275	280	285				
Leu Val Val Asp Gly Val Lys Leu Ile Pro Leu Pro Ile Thr Val Ala						
290	295	300				

Cys Ser Ala Ala Ile Ser Gly Ala Leu Thr Ala Ala Ser Ala Gly Ile  
 305 310 315 320  
 Gly Leu Tyr Ser Ile Trp Gln Lys Thr Lys Ser Gly Lys  
 325 330

<210> 293  
 <211> 7  
 <212> DNA  
 <213> Chlamydia

<400> 293  
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<210> 294  
 <211> 196  
 <212> PRT  
 <213> Chlamydia

<400> 294  
 Thr Met Gly Ser Leu Val Gly Arg Gln Ala Pro Asp Phe Ser Gly Lys  
 5 10 15

Ala Val Val Cys Gly Glu Glu Lys Glu Ile Ser Leu Ala Asp Phe Arg  
 20 25 30

Gly Lys Tyr Val Val Leu Phe Phe Tyr Pro Lys Asp Phe Thr Tyr Val  
 35 40 45

Cys Pro Thr Glu Leu His Ala Phe Gln Asp Arg Leu Val Asp Phe Glu  
 50 55 60

Glu His Gly Ala Val Val Leu Gly Cys Ser Val Asp Asp Ile Glu Thr  
 65 70 75 80

His Ser Arg Trp Leu Thr Val Ala Arg Asp Ala Gly Gly Ile Glu Gly  
 85 90 95

Thr Glu Tyr Pro Leu Leu Ala Asp Pro Ser Phe Lys Ile Ser Glu Ala  
 100 105 110

Phe Gly Val Leu Asn Pro Glu Gly Ser Leu Ala Leu Arg Ala Thr Phe  
 115 120 125

Leu Ile Asp Lys His Gly Val Ile Arg His Ala Val Ile Asn Asp Leu  
 130 135 140

Pro Leu Gly Arg Ser Ile Asp Glu Glu Leu Arg Ile Leu Asp Ser Leu  
 145 150 155 160

Ile Phe Phe Glu Asn His Gly Met Val Cys Pro Ala Asn Trp Arg Ser  
 165 170 175

Gly Glu Arg Gly Met Val Pro Ser Glu Glu Gly Leu Lys Glu Tyr Phe  
 180 185 190

Gln Thr Met Asp  
195

<210> 295

<211> 181

<212> PRT

<213> Chlamydia

<400> 295  
Lys Gly Gly Lys Met Ser Thr Thr Ile Ser Gly Asp Ala Ser Ser Leu  
5 10 15

Pro Leu Pro Thr Ala Ser Cys Val Glu Thr Lys Ser Thr Ser Ser Ser  
20 25 30

Thr Lys Gly Asn Thr Cys Ser Lys Ile Leu Asp Ile Ala Leu Ala Ile  
35 40 45

Val Gly Ala Leu Val Val Val Ala Gly Val Leu Ala Leu Val Leu Cys  
50 55 60

Ala Ser Asn Val Ile Phe Thr Val Ile Gly Ile Pro Ala Leu Ile Ile  
65 70 75 80

Gly Ser Ala Cys Val Gly Ala Gly Ile Ser Arg Leu Met Tyr Arg Ser  
85 90 95

Ser Tyr Ala Ser Leu Glu Ala Lys Asn Val Leu Ala Glu Gln Arg Leu  
100 105 110

Arg Asn Leu Ser Glu Glu Lys Asp Ala Leu Ala Ser Val Ser Phe Ile  
115 120 125

Asn Lys Met Phe Leu Arg Gly Leu Thr Asp Asp Leu Gln Ala Leu Glu  
130 135 140

Ala Lys Val Met Glu Phe Glu Ile Asp Cys Leu Asp Arg Leu Glu Lys  
145 150 155 160

Asn Glu Gln Ala Leu Leu Ser Asp Val Arg Leu Val Leu Ser Ser Tyr  
165 170 175

Thr Arg Trp Leu Asp  
180

<210> 296

<211> 124

<212> PRT

<213> Chlamydia

<400> 296  
Ile Tyr Glu Val Met Asn Met Asp Leu Glu Thr Arg Arg Ser Phe Ala  
5 10 15

Val Gln Gln Gly His Tyr Gln Asp Pro Arg Ala Ser Asp Tyr Asp Leu  
20 25 30

Pro Arg Ala Ser Asp Tyr Asp Leu Pro Arg Ser Pro Tyr Pro Thr Pro  
35 40 45

Pro Leu Pro Ser Arg Tyr Gln Leu Gln Asn Met Asp Val Glu Ala Gly  
50 55 60

Phe Arg Glu Ala Val Tyr Ala Ser Phe Val Ala Gly Met Tyr Asn Tyr  
65 70 75 80

Val Val Thr Gln Pro Gln Glu Arg Ile Pro Asn Ser Gln Gln Val Glu  
85 90 95

Gly Ile Leu Arg Asp Met Leu Thr Asn Gly Ser Gln Thr Phe Ser Asn  
100 105 110

Leu Met Gln Arg Trp Asp Arg Glu Val Asp Arg Glu  
115 120

<210> 297

<211> 488

<212> PRT

<213> Chlamydia

<400> 297

Lys Gly Ser Leu Pro Ile Leu Gly Pro Phe Leu Asn Gly Lys Met Gly  
5 10 15

Phe Trp Arg Thr Ser Ile Met Lys Met Asn Arg Ile Trp Leu Leu Leu  
20 25 30

Leu Thr Phe Ser Ser Ala Ile His Ser Pro Val Arg Gly Glu Ser Leu  
35 40 45

Val Cys Lys Asn Ala Leu Gln Asp Leu Ser Phe Leu Glu His Leu Leu  
50 55 60

Gln Val Lys Tyr Ala Pro Lys Thr Trp Lys Glu Gln Tyr Leu Gly Trp  
65 70 75 80

Asp Leu Val Gln Ser Ser Val Ser Ala Gln Gln Lys Leu Arg Thr Gln  
85 90 95

Glu Asn Pro Ser Thr Ser Phe Cys Gln Gln Val Leu Ala Asp Phe Ile  
100 105 110

Gly Gly Leu Asn Asp Phe His Ala Gly Val Thr Phe Phe Ala Ile Glu  
115 120 125

Ser Ala Tyr Leu Pro Tyr Thr Val Gln Lys Ser Ser Asp Gly Arg Phe  
130 135 140

Tyr Phe Val Asp Ile Met Thr Phe Ser Ser Glu Ile Arg Val Gly Asp  
 145 150 155 160  
 Glu Leu Leu Glu Val Asp Gly Ala Pro Val Gln Asp Val Leu Ala Thr  
 165 170 175  
 Leu Tyr Gly Ser Asn His Lys Gly Thr Ala Ala Glu Ser Ala Ala  
 180 185 190  
 Leu Arg Thr Leu Phe Ser Arg Met Ala Ser Leu Gly His Lys Val Pro  
 195 200 205  
 Ser Gly Arg Thr Thr Leu Lys Ile Arg Arg Pro Phe Gly Thr Thr Arg  
 210 215 220  
 Glu Val Arg Val Lys Trp Arg Tyr Val Pro Glu Gly Val Gly Asp Leu  
 225 230 235 240  
 Ala Thr Ile Ala Pro Ser Ile Arg Ala Pro Gln Leu Gln Lys Ser Met  
 245 250 255  
 Arg Ser Phe Phe Pro Lys Lys Asp Asp Ala Phe His Arg Ser Ser Ser  
 260 265 270  
 Leu Phe Tyr Ser Pro Met Val Pro His Phe Trp Ala Glu Leu Arg Asn  
 275 280 285  
 His Tyr Ala Thr Ser Gly Leu Lys Ser Gly Tyr Asn Ile Gly Ser Thr  
 290 295 300  
 Asp Gly Phe Leu Pro Val Ile Gly Pro Val Ile Trp Glu Ser Glu Gly  
 305 310 315 320  
 Leu Phe Arg Ala Tyr Ile Ser Ser Val Thr Asp Gly Asp Gly Lys Ser  
 325 330 335  
 His Lys Val Gly Phe Leu Arg Ile Pro Thr Tyr Ser Trp Gln Asp Met  
 340 345 350  
 Glu Asp Phe Asp Pro Ser Gly Pro Pro Pro Trp Glu Glu Phe Ala Lys  
 355 360 365  
 Ile Ile Gln Val Phe Ser Ser Asn Thr Glu Ala Leu Ile Ile Asp Gln  
 370 375 380  
 Thr Asn Asn Pro Gly Gly Ser Val Leu Tyr Leu Tyr Ala Leu Leu Ser  
 385 390 395 400  
 Met Leu Thr Asp Arg Pro Leu Glu Leu Pro Lys His Arg Met Ile Leu  
 405 410 415  
 Thr Gln Asp Glu Val Val Asp Ala Leu Asp Trp Leu Thr Leu Leu Glu  
 420 425 430

Asn Val Asp Thr Asn Val Glu Ser Arg Leu Ala Leu Gly Asp Asn Met  
435 440 445

Glu Gly Tyr Thr Val Asp Leu Gln Val Ala Glu Tyr Leu Lys Ser Phe  
450 455 460

Gly Arg Gln Val Leu Asn Cys Trp Ser Lys Gly Asp Ile Glu Leu Ser  
465 470 475 480

Thr Pro Ile Pro Leu Phe Gly Phe  
485

<210> 298

<211> 140

<212> PRT

<213> Chlamydia

<400> 298

Arg Ile Asp Ile Ser Ser Val Thr Phe Phe Ile Gly Ile Leu Leu Ala  
5 10 15

Val Asn Ala Leu Thr Tyr Ser His Val Leu Arg Asp Leu Ser Val Ser  
20 25 30

Met Asp Ala Leu Phe Ser Arg Asn Thr Leu Ala Val Leu Leu Gly Leu  
35 40 45

Val Ser Ser Val Leu Asp Asn Val Pro Leu Val Ala Ala Thr Ile Gly  
50 55 60

Met Tyr Asp Leu Pro Met Asn Asp Pro Leu Trp Lys Leu Ile Ala Tyr  
65 70 75 80

Thr Ala Gly Thr Gly Gly Ser Ile Leu Ile Ile Gly Ser Ala Ala Gly  
85 90 95

Val Ala Tyr Met Gly Met Glu Lys Val Ser Phe Gly Trp Tyr Val Lys  
100 105 110

His Ala Ser Trp Ile Ala Leu Ala Ser Tyr Phe Gly Gly Leu Ala Val  
115 120 125

Tyr Phe Leu Met Glu Asn Cys Val Asn Leu Phe Val  
130 135 140

<210> 299

<211> 361

<212> PRT

<213> Chlamydia

<400> 299

His Gln Glu Ile Ala Asp Ser Pro Leu Val Lys Lys Ala Glu Glu Gln  
5 10 15

Ile Asn Gln Ala Gln Gln Asp Ile Gln Thr Ile Thr Pro Ser Gly Leu  
 20 25 30  
 Asp Ile Pro Ile Val Gly Pro Ser Gly Ser Ala Ala Ser Ala Gly Ser  
 35 40 45  
 Ala Ala Gly Ala Leu Lys Ser Ser Asn Asn Ser Gly Arg Ile Ser Leu  
 50 55 60  
 Leu Leu Asp Asp Val Asp Asn Glu Met Ala Ala Ile Ala Met Gln Gly  
 65 70 75 80  
 Phe Arg Ser Met Ile Glu Gln Phe Asn Val Asn Asn Pro Ala Thr Ala  
 85 90 95  
 Lys Glu Leu Gln Ala Met Glu Ala Gln Leu Thr Ala Met Ser Asp Gln  
 100 105 110  
 Leu Val Gly Ala Asp Gly Glu Leu Pro Ala Glu Ile Gln Ala Ile Lys  
 115 120 125  
 Asp Ala Leu Ala Gln Ala Leu Lys Gln Pro Ser Ala Asp Gly Leu Ala  
 130 135 140  
 Thr Ala Met Gly Gln Val Ala Phe Ala Ala Lys Val Gly Gly Gly  
 145 150 155 160  
 Ser Ala Gly Thr Ala Gly Thr Val Gln Met Asn Val Lys Gln Leu Tyr  
 165 170 175  
 Lys Thr Ala Phe Ser Ser Thr Ser Ser Ser Tyr Ala Ala Ala Leu  
 180 185 190  
 Ser Asp Gly Tyr Ser Ala Tyr Lys Thr Leu Asn Ser Leu Tyr Ser Glu  
 195 200 205  
 Ser Arg Ser Gly Val Gln Ser Ala Ile Ser Gln Thr Ala Asn Pro Ala  
 210 215 220  
 Leu Ser Arg Ser Val Ser Arg Ser Gly Ile Glu Ser Gln Gly Arg Ser  
 225 230 235 240  
 Ala Asp Ala Ser Gln Arg Ala Ala Glu Thr Ile Val Arg Asp Ser Gln  
 245 250 255  
 Thr Leu Gly Asp Val Tyr Ser Arg Leu Gln Val Leu Asp Ser Leu Met  
 260 265 270  
 Ser Thr Ile Val Ser Asn Pro Gln Ala Asn Gln Glu Glu Ile Met Gln  
 275 280 285  
 Lys Leu Thr Ala Ser Ile Ser Lys Ala Pro Gln Phe Gly Tyr Pro Ala  
 290 295 300

Val Gln Asn Ser Val Asp Ser Leu Gln Lys Phe Ala Ala Gln Leu Glu  
 305                   310                   315                   320  
  
 Arg Glu Phe Val Asp Gly Glu Arg Ser Leu Ala Glu Ser Gln Glu Asn  
 325                   330                   335  
  
 Ala Phe Arg Lys Gln Pro Ala Phe Ile Gln Gln Val Leu Val Asn Ile  
 340                   345                   350  
  
 Ala Ser Leu Phe Ser Gly Tyr Leu Ser  
 355                   360  
  
 <210> 300  
 <211> 207  
 <212> PRT  
 <213> Chlamydia  
  
 <400> 300  
 Ser Ser Lys Ile Val Ser Leu Cys Glu Gly Ala Val Ala Asp Ala Arg  
 5                   10                   15  
  
 Met Cys Lys Ala Glu Leu Ile Lys Lys Glu Ala Asp Ala Tyr Leu Phe  
 20                   25                   30  
  
 Cys Glu Lys Ser Gly Ile Tyr Leu Thr Lys Lys Glu Gly Ile Leu Ile  
 35                   40                   45  
  
 Pro Ser Ala Gly Ile Asp Glu Ser Asn Thr Asp Gln Pro Phe Val Leu  
 50                   55                   60  
  
 Tyr Pro Lys Asp Ile Leu Gly Ser Cys Asn Arg Ile Gly Glu Trp Leu  
 65                   70                   75                   80  
  
 Arg Asn Tyr Phe Arg Val Lys Glu Leu Gly Val Ile Ile Thr Asp Ser  
 85                   90                   95  
  
 His Thr Thr Pro Met Arg Arg Gly Val Leu Gly Ile Gly Leu Cys Trp  
 100                  105                  110  
  
 Tyr Gly Phe Ser Pro Leu His Asn Tyr Ile Gly Ser Leu Asp Cys Phe  
 115                  120                  125  
  
 Gly Arg Pro Leu Gln Met Thr Gln Ser Asn Leu Val Asp Ala Leu Ala  
 130                  135                  140  
  
 Val Ala Ala Val Val Cys Met Gly Glu Gly Asn Glu Gln Thr Pro Leu  
 145                  150                  155                  160  
  
 Ala Val Ile Glu Gln Ala Pro Asn Met Val Tyr His Ser Tyr Pro Thr  
 165                  170                  175  
  
 Ser Arg Glu Glu Tyr Cys Ser Leu Arg Ile Asp Glu Thr Glu Asp Leu  
 180                  185                  190

Tyr Gly Pro Phe Leu Gln Ala Val Thr Trp Ser Gln Glu Lys Lys  
 195 200 205

<210> 301  
 <211> 183  
 <212> PRT  
 <213> Chlamydia

<400> 301  
 Ile Pro Pro Ala Pro Arg Gly His Pro Gln Ile Glu Val Thr Phe Asp  
 5 10 15  
 Ile Asp Ala Asn Gly Ile Leu His Val Ser Ala Lys Asp Ala Ala Ser  
 20 25 30  
 Gly Arg Glu Gln Lys Ile Arg Ile Glu Ala Ser Ser Gly Leu Lys Glu  
 35 40 45  
 Asp Glu Ile Gln Gln Met Ile Arg Asp Ala Glu Leu His Lys Glu  
 50 55 60  
 Asp Lys Gin Arg Lys Glu Ala Ser Asp Val Lys Asn Glu Ala Asp Gly  
 65 70 75 80  
 Met Ile Phe Arg Ala Glu Lys Ala Val Lys Asp Tyr His Asp Lys Ile  
 85 90 95  
 Pro Ala Glu Leu Val Lys Glu Ile Glu Glu His Ile Glu Lys Val Arg  
 100 105 110  
 Gln Ala Ile Lys Glu Asp Ala Ser Thr Thr Ala Ile Lys Ala Ala Ser  
 115 120 125  
 Asp Glu Leu Ser Thr Arg Met Gln Lys Ile Gly Glu Ala Met Gln Ala  
 130 135 140  
 Gln Ser Ala Ser Ala Ala Ser Ser Ala Ala Asn Ala Gln Gly Gly  
 145 150 155 160  
 Pro Asn Ile Asn Ser Glu Asp Leu Lys Lys His Ser Phe Ser Thr Arg  
 165 170 175  
 Pro Pro Ala Gly Gly Ser Ala  
 180

<210> 302  
 <211> 232  
 <212> PRT  
 <213> Chlamydia

<400> 302  
 Met Thr Lys His Gly Lys Arg Ile Arg Gly Ile Gln Glu Thr Tyr Asp  
 5 10 15

Leu Ala Lys Ser Tyr Ser Leu Gly Glu Ala Ile Asp Ile Leu Lys Gln  
20 25 30

Cys Pro Thr Val Arg Phe Asp Gln Thr Val Asp Val Ser Val Lys Leu  
35 40 45

Gly Ile Asp Pro Arg Lys Ser Asp Gln Gln Ile Arg Gly Ser Val Ser  
50 55 60

Leu Pro His Gly Thr Gly Lys Val Leu Arg Ile Leu Val Phe Ala Ala  
65 70 75 80

Gly Asp Lys Ala Ala Glu Ala Ile Glu Ala Gly Ala Asp Phe Val Gly  
85 90 95

Ser Asp Asp Leu Val Glu Lys Ile Lys Gly Gly Trp Val Asp Phe Asp  
100 105 110

Val Ala Val Ala Thr Pro Asp Met Met Arg Glu Val Gly Lys Leu Gly  
115 120 125

Lys Val Leu Gly Pro Arg Asn Leu Met Pro Thr Pro Lys Ala Gly Thr  
130 135 140

Val Thr Thr Asp Val Val Lys Thr Ile Ala Glu Leu Arg Lys Gly Lys  
145 150 155 160

Ile Glu Phe Lys Ala Asp Arg Ala Gly Val Cys Asn Val Gly Val Ala  
165 170 175

Lys Leu Ser Phe Asp Ser Ala Gln Ile Lys Glu Asn Val Glu Ala Leu  
180 185 190

Cys Ala Ala Leu Val Lys Ala Lys Pro Ala Thr Ala Lys Gly Gln Tyr  
195 200 205

Leu Val Asn Phe Thr Ile Ser Ser Thr Met Gly Pro Gly Val Thr Val  
210 215 220

Asp Thr Arg Glu Leu Ile Ala Leu  
225 230

<210> 303

<211> 238

<212> PRT

<213> chlamydia

<400> 303

Ile Asn Ser Lys Leu Glu Thr Lys Asn Leu Ile Tyr Leu Lys Leu Lys  
5 10 15

Ile Lys Lys Ser Phe Lys Met Gly Asn Ser Gly Phe Tyr Leu Tyr Asn  
20 25 30

Thr Gln Asn Cys Val Phe Ala Asp Asn Ile Lys Val Gly Gln Met Thr  
 35 40 45  
 Glu Pro Leu Lys Asp Gln Gln Ile Ile Leu Gly Thr Thr Ser Thr Pro  
 50 55 60  
 Val Ala Ala Lys Met Thr Ala Ser Asp Gly Ile Ser Leu Thr Val Ser  
 65 70 75 80  
 Asn Asn Pro Ser Thr Asn Ala Ser Ile Thr Ile Gly Leu Asp Ala Glu  
 85 90 95  
 Lys Ala Tyr Gln Leu Ile Leu Glu Lys Leu Gly Asp Gln Ile Leu Gly  
 100 105 110  
 Gly Ile Ala Asp Thr Ile Val Asp Ser Thr Val Gln Asp Ile Leu Asp  
 115 120 125  
 Lys Ile Thr Thr Asp Pro Ser Leu Gly Leu Leu Lys Ala Phe Asn Asn  
 130 135 140  
 Phe Pro Ile Thr Asn Lys Ile Gln Cys Asn Gly Leu Phe Thr Pro Arg  
 145 150 155 160  
 Asn Ile Glu Thr Leu Leu Gly Thr Glu Ile Gly Lys Phe Thr Val  
 165 170 175  
 Thr Pro Lys Ser Ser Gly Ser Met Phe Leu Val Ser Ala Asp Ile Ile  
 180 185 190  
 Ala Ser Arg Met Glu Gly Gly Val Val Leu Ala Leu Val Arg Glu Gly  
 195 200 205  
 Asp Ser Lys Pro Tyr Ala Ile Ser Tyr Gly Tyr Ser Ser Gly Val Pro  
 210 215 220  
 Asn Leu Cys Ser Leu Arg Thr Arg Ile Ile Asn Thr Gly Leu  
 225 230 235

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